

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 15:26:43 ; Search time 154 Seconds  
(without alignments)  
423.953 Million cell updates/sec

Title: US-09-602-597A-4  
Perfect score: 930  
Sequence: 1 MAEPFVKVSTRTSSPAQAE.....QAWRGVCSNAATSQMAGGYA 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2000s: \*  
5: Geneseqp2000s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	100.0	182	3	AAY70458 Human men
2	930	100.0	182	8	Adn04054 Antipsori
3	930	100.0	182	8	Ado55157 Protein #
4	930	100.0	216	4	AAB61164 Human BBS
5	848	91.2	182	2	AAR99799 NTII-11 n
6	825	67.2	125	5	Abb90064 Human pol
7	580	62.4	113	3	AAB34711 Human sec
8	580	62.4	113	3	Abb90110 Human pol
9	325	34.9	173	3	AAY53643 A bone ma
10	322	34.6	173	4	AAM25799 Human pro
11	307	33.0	153	2	Aaw52117 Human pro
12	283	30.4	132	5	Abp41095 Human ova
13	206.5	22.2	527	4	ABG15862 Novel hum
14	191	20.5	100	6	Adas7177 Human sec
15	191	20.5	100	6	Ada41044 Human sec
16	191	20.5	100	6	Abt47899 Human sec
17	191	20.5	100	7	Adc74294 Human sec
18	191	20.5	101	2	AAY41391 Human sec
19	183	19.7	145	4	Aao12388 Human tra
20	162	17.4	176	4	Aab82597 Human gen
21	162	17.4	176	4	Aae03822 Human gen
22	162	17.4	176	5	Abp69675 Human pol
23	162	17.4	176	5	ABG96412 Human ova
24	162	17.4	176	5	ABG64565 Human alb
25	162	17.4	176	6	Abj37034 Human bre

26	162	17.4	176	8	ADL77832	Adl77832 Albumin f
27	162	17.4	176	8	ADL26758	Adl26758 Human MAL
28	162	17.4	215	5	ABP41741	Abp41741 Human ova
29	153	16.5	153	4	ABE50292	Abb50292 T cell di
30	153	16.5	153	7	AD49049	Ada49049 Human NOV
31	153	16.5	153	8	ADK67352	Adk67352 Human MAL
32	148.5	16.0	148	4	AAB90802	Aab90802 Human she
33	148.5	16.0	148	4	AAB76862	Aab76862 Human lun
34	148.5	16.0	148	5	AAU85517	Aau85517 Clone #18
35	148.5	16.0	148	6	ABU69489	Abu69489 Human lun
36	148.5	16.0	148	6	ABU66391	Abu66391 Lung canc
37	148.5	16.0	148	7	ADH45857	Adh45857 Human lun
38	148.5	16.0	148	7	ADH45857	Adh45857 Human lun
39	148.5	16.0	153	5	ABP64884	Abp64884 Human pro
40	148.5	16.0	153	8	ADJ75560	Adj75560 Marker ge
41	148.5	16.0	153	8	ADNO6014	Adno6014 Antipsori
42	148.5	16.0	153	8	ADNO4421	Adno4421 Antipsori
43	148.5	16.0	169	3	AA856719	Aab56719 Human pro
44	147.5	15.9	265	4	AA849502	Aab49502 Clone HVA
45	146	15.7	143	7	ADE72397	Ade72397 Human end

ALIGNMENTS

RESULT 1  
AAY70458  
ID AAY70458 standard; protein; 182 AA.  
XX AC AAY70458;  
XX 21-JUN-2000 (first entry)  
DT Human membrane channel protein-8 (MECHP-8).  
DE  
XX

Membrane channel protein-8; MECHP-8; diagnosis; treatment; lymphoma;  
cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;  
inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;  
diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;  
muscular disorder; myocarditis; Duchenne's muscular dystrophy; noctropic;  
cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiac;  
neurological disorder; Alzheimer's disease; Parkinson's disease; human;  
Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;  
anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;  
hypotensive; vasotropic; antiaschmatic; antiinflammatory; antidepressant;  
anticonvulsant; thrombolytic; antiparkinsonian; immunostimulant.

Key	Location/Qualifiers
Modified-site	/note= "Phosphorylation site"
Domain	/label= Transmembrane_domain
Domain	/label= Transmembrane_domain
Domain	/label= Transmembrane_domain
Modified-site	/note= "Glycosylation site"
Modified-site	/note= "Phosphorylation site"

WO200012711-A2.

09-MAR-2000.

02-SEP-1999; 99WO-US020468.

02-SEP-1998; 98US-0155226P.

12-NOV-1998; 98US-00191283.

09-DEC-1998; 98US-0155225P.

26-JAN-1999; 99US-0155211P.

PR 10-FEB-1999; 99US-0155263P.  
 XX (INCY-) INCYTE PHARM INC.  
 PA Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;  
 PI Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Aizimzai Y;  
 XX WPI; 2000-256643/22.  
 DR N-PSDB; AAZ51624.  
 XX Novel human membrane channel protein and polynucleotide useful for  
 PT diagnosing and treating cell proliferative, inflammatory, secretory,  
 PT osmoregulatory, muscular, cardiovascular and neurological disorders.  
 XX Claim 1; Page 107; 140pp; English.  
 PS The present sequence is the human membrane channel protein-8 (MECHP-8),  
 CC which is expressed in nervous and gastrointestinal tissues. Anti-MECHP  
 CC antibodies can be used as therapeutic antagonists and reagents for  
 CC diagnosis and monitoring diseases. MECHP cDNA can be used for diagnosis  
 CC of MECHP-related diseases and gene mapping. MECHP can be used for  
 CC treatment of cell proliferative disorders such as bursitis and  
 CC atherosclerosis, cancers like lymphoma and sarcoma, inflammatory  
 CC disorders like AIDS and Addison's disease, transport/secretory disorders  
 CC like cystic fibrosis and diabetes mellitus, osmoregulatory disorders like  
 CC diarrhoea and renal failure, muscular disorders like myocarditis and  
 CC Duchenne's muscular dystrophy, cardiovascular disorders like hypertension  
 CC and vasculitis, congenital lung anomalies like bronchitis and asthma and  
 CC neurological disorders like Alzheimer's disease, Parkinson's disease and  
 XX Huntington's disease  
 XX Sequence 182 AA;  
 SQ Query Match 100.0%; Score 930; DB 3; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-106;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEFPKSVTRTSSPAQGAASVSALRPLDGFVRSRLGALMLLQVLGLLVWALIADTFY 60  
 DB 1 MAEFPKSVTRTSSPAQGAASVSALRPLDGFVRSRLGALMLLQVLGLLVWALIADTFY 60  
 QY 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMIFNISATVLYITAFI 120  
 DB 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMIFNISATVLYITAFI 120  
 QY 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180  
 DB 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180  
 QY 181 YA 182  
 DB 181 YA 182  
 RESULT 2  
 ID ADN04054 standard; protein; 182 AA.  
 XX AC ADN04054;  
 XX 01-JUL-2004 (first entry)  
 XX Antipsoriatic protein sequence #222.  
 XX antipsoriatic; gene therapy; psoriasis; diagnosis.  
 OS Homo sapiens.  
 XX WO2004028479-A2.  
 XX 08-APR-2004.  
 XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.  
 XX (GETH ) GENENTECH INC.  
 PA Bodary S, Clark H, Jackman J, Schoenfeld J, Williams FM, Wood WI;  
 PI Wu TD;  
 XX WPI; 2004-305105/28.  
 DR N-PSDB; ADN04053.  
 XX New PRO nucleic acid or polypeptide, useful for preparing a  
 PT pharmaceutical composition for diagnosing or treating psoriasis in a  
 PT mammal.  
 XX Claim 9; SEQ ID NO 448; 3069pp; English.  
 XX The invention relates to novel polynucleotide and polypeptides for  
 CC treating psoriasis or a sequence having at least 80% identity to the  
 CC above sequences. The nucleic acid is useful for preparing a composition  
 CC for diagnosing or treating psoriasis in a mammal. This sequence  
 CC corresponds to one of the polypeptides of the invention.  
 XX Sequence 182 AA;  
 SQ Query Match 100.0%; Score 930; DB 8; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-106;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAEFPKSVTRTSSPAQGAASVSALRPLDGFVRSRLGALMLLQVLGLLVWALIADTFY 60  
 DB 1 MAEFPKSVTRTSSPAQGAASVSALRPLDGFVRSRLGALMLLQVLGLLVWALIADTFY 60  
 QY 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMIFNISATVLYITAFI 120  
 DB 61 HLYPAYGWNMFVAVFLWLVTVILFNLVLFQHLKMLYMPWPLVLMIFNISATVLYITAFI 120  
 QY 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180  
 DB 121 ACSAAVDLTSRLGTRFPYNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGG 180  
 QY 181 YA 182  
 DB 181 YA 182  
 RESULT 3  
 ID ADO55157 standard; protein; 182 AA.  
 XX AC ADO55157;  
 XX 15-JUL-2004 (first entry)  
 XX Protein #59 with increased gene expression in renal cell carcinoma.  
 XX cytostatic; gene therapy; differential expression; renal cell carcinoma;  
 XX clear cell RCC; papillary RCC; chromophobe/oncocytoma RCC;  
 XX sarcomatoid RCC; TCC; Wilms' tumor; gene expression; kidney cancer;  
 XX diagnostic marker; cancer.  
 OS Homo sapiens.  
 XX WO2004032842-A2.  
 XX 22-APR-2004.  
 XX 06-OCT-2003; 2003WO-US031476.  
 XX 04-OCT-2002; 2002US-0415775P.  
 XX (VAND-) VAN ANDEL INST.  
 XX

```

PI    Teh BT, Takahashi M;
XX
DR    WPI; 2004-340789/31.
XX
DR    N-PSDB; RDO54972.
XX
PI    New nucleic acid and polypeptide compositions, useful in the field of
XX    molecular biology and medicine, in particular for gene expression
XX    profiling, identifying diagnostic markers, and treating certain types of
XX    kidney cancer.
XX
PS    Example IV; SEQ ID NO 254; 53pp; English.
XX
CC    The invention relates to novel genes that are differentially expressed in
XX    sub-types of renal cell carcinomas and methods of detecting them using
XX    nucleic acids and probes. The nucleic acid probes hybridize with part or
XX    all of a coding sequence that is overexpressed in clear cell renal cell
XX    carcinoma (CC-RCC), papillary RCC, chromophobe/oncocytoma RCC,
XX    sarcomatoid RCC, TCC, or Wilms' tumors, which overexpression is based on
XX    comparison to a baseline value. The methods and compositions of the
XX    present invention are useful in the field of molecular biology and
XX    medicine, in particular for gene expression profiling of certain types of
XX    kidney cancer, in identifying diagnostic markers, and treating such
XX    cancer patients. This sequence corresponds to the protein encoded by a
XX    gene with increased expression in CC-RCC.
XX
SQ    Sequence 182 AA;
      Query Match          100.0%; Score 930; DB 8; Length 182;
      Best Local Similarity 100.0%; Pred. No. 1.1e-106;
      Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      Qy 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSLGALMLLQLVLGLVWALIADTPY 60
      Db 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSLGALMLLQLVLGLVWALIADTPY 60
      Qy 61 HLYPAYGWMVFAVFLWLVTLVFNLYLFQHLHKLVMVWPVLVMTFNISATVLYITAFI 120
      Db 61 HLYPAYGWMVFAVFLWLVTLVFNLYLFQHLHKLVMVWPVLVMTFNISATVLYITAFI 120
      Qy 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
      Db 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
      Qy 181 YA 182
      Db 181 YA 182
      RESULT 4
      AAB61164
      ID AAB61164 standard; protein; 216 AA.
      AC AAB61164;
      XX
      XX 02-APR-2001 (first entry)
      XX
      XX Human BBSR PLP protein.
      XX
      XX Human; BBSR; Bardet-Biedl Syndrome Region; PLP; plasmalipin-like protein;
      XX    antidiabetic; anorectic; ophthalmological; antiinflammatory; nootropic;
      XX    cardiant; nephrotropic; gene therapy; chromosome 16;
      XX    retinal degeneration; hypogenitalism; polydactyly; brachydactyly;
      XX    obesity; mental retardation; renal disorder; diabetes;
      XX    cardiovascular disorder.
      XX
      XX Homo sapiens.
      XX
      XX WO200100825-A2.
      XX
      XX 04-JAN-2001.
      XX
      XX 22-JUN-2000; 2000WO-US017375.
      XX

```

```

PR    30-JUN-1999; 99US-0141753P.
XX
XX (CHIR ) CHIRON CORP.
XX
PI    Duhl D, Gorman SW;
XX
DR    WPI; 2001-123009/13.
XX
DR    N-PSDB; AAF28357.
XX
XX New human chromosome 15 and 16 Bardet-Biedl Syndrome Region polypeptide
XX    and polynucleotide for diagnosis and treatment of obesity, retinal
XX    degeneration, mental retardation, nervous system, heart and kidney
XX    disorders.
XX
XX Claim 10; Fig 2; Sipp; English.
XX
XX The present sequence is encoded by one of five novel Bardet-Biedl
XX    Syndrome Region (BBSR) polynucleotides that map to human chromosome 15 or
XX    16. BBSR polynucleotides, polypeptides and anti-BBSR antibodies are
XX    useful for treating a BBSR protein-modulated disorder in a subject. An
XX    antibody that specifically binds to a BBSR protein is useful for
XX    diagnosing a BBSR protein-modulated disorder. BBSR protein-modulated
XX    disorders include Bardet-Biedl syndrome, retinal degeneration including
XX    retinitis pigmentosa, hypogenitalism, polydactyly, brachydactyly,
XX    obesity, mental retardation, renal abnormalities, diabetes and
XX    cardiovascular abnormalities. BBSR polypeptides are also useful for
XX    screening combinatorial libraries to identify agonist or antagonists.
XX    Antibodies against BBSR polypeptides are useful for affinity
XX    chromatography, for distinguishing BBSR polypeptides and for inhibiting
XX    or modulating an activity or biological effect or a disorder associated
XX    with the BBSR proteins
XX
SQ    Sequence 216 AA;
      Query Match          100.0%; Score 930; DB 4; Length 216;
      Best Local Similarity 100.0%; Pred. No. 1.4e-106;
      Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      Qy 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSLGALMLLQLVLGLVWALIADTPY 60
      Db 1 MAEFPKSVTRTSSPAQGAASVSALRDPDLGFRSLGALMLLQLVLGLVWALIADTPY 60
      Qy 61 HLYPAYGWMVFAVFLWLVTLVFNLYLFQHLHKLVMVWPVLVMTFNISATVLYITAFI 120
      Db 61 HLYPAYGWMVFAVFLWLVTLVFNLYLFQHLHKLVMVWPVLVMTFNISATVLYITAFI 120
      Qy 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
      Db 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSFFSYQAWRGVGSNAATSQMAGG 180
      Qy 181 YA 182
      Db 181 YA 182
      RESULT 5
      AAR99799
      ID AAR99799 standard; protein; 182 AA.
      XX
      XX AAR99799;
      AC AAR99799;
      DT 25-MAR-2003 (revised)
      DT 02-JAN-1997 (first entry)
      XX
      XX NTII-11 nerve protein, facilitates regeneration of nerve cells.
      XX
      XX Probe; central nervous system; peripheral nervous system; CNS; PNS; axon;
      XX    neurone; neuronal cells; glial cells; Schwann cells; trauma; pathology;
      XX    regeneration; MS2; metalloprotease.
      XX
      XX Homo sapiens.
      XX
      XX WO9617865-A2.
      XX

```



XX DE Human secreted protein encoded by DNA clone v06.1.  
 XX KW Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;  
 XX KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;  
 XX KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;  
 XX KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;  
 XX KW contraceptive; infection; growth inhibition; hyperproliferative disorder;  
 XX KW psoriasis.  
 XX OS Homo sapiens.  
 XX PN WO200055375-A1.  
 XX PD 21-SEP-2000.  
 XX PF 17-MAR-2000; 2000WO-US007285.  
 XX PR 17-MAR-1999; 99US-0124808P.  
 XX PR 17-MAR-1999; 99US-0124916P.  
 XX PR 17-AUG-1999; 99US-0149639P.  
 XX PR 01-OCT-1999; 99US-0157247P.  
 XX PR 29-NOV-1999; 99US-0167824P.  
 XX PR 15-FEB-2000; 2000US-0182711P.  
 XX PA (ALPH-) ALPHAGENE INC.  
 XX PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;  
 XX DR WPI; 2000-638211/61.  
 XX DR N-PSDB; AAC59812.  
 XX PT Novel proteins and polypeptides useful for the treatment of e.g multiple  
 XX PT sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer,  
 XX PT Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers.  
 XX PS Claim 58; Page 419; 493pp; English.  
 XX CC This invention relates to 59 human secreted proteins and the nucleotide  
 XX CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745  
 XX CC represent the proteins and their encoding nucleotide sequences, and  
 XX CC sequences AAB34746-B34771 represent fragments of the proteins. Probes for  
 XX CC the DNA sequences are represented by sequences AAC59847-C59996. The  
 XX CC proteins exhibit neuroprotective, dermatological, immunosuppressive,  
 XX CC antiinflammatory, antianaemic, neurotropic, antiparkinsonian,  
 XX CC cerebroprotective, haemostatic, vulnary, cytostatic, antipsoriatic,  
 XX CC antibacterial, virucide, and fungicide activity. The proteins and  
 XX CC nucleotide sequences are useful as nutritional sources or supplements and  
 XX CC in research. The proteins are useful for treating immune deficiency and  
 XX CC disorders, which may be genetic or resulting from infections, autoimmune  
 XX CC disorders such as multiple sclerosis, systemic lupus erythematosus,  
 XX CC rheumatoid arthritis, and for treating myeloid or lymphoid cell  
 XX CC deficiencies such as anaemias by regulating haematopoiesis. The proteins  
 XX CC are also useful in compositions for bone, cartilage, tendon, ligament  
 XX CC and/or nerve tissue growth or regeneration, for wound healing, tissue  
 XX CC repair and replacement and in the treatment of wounds, incisions and  
 XX CC ulcers. Other uses include in the treatment of central and peripheral  
 XX CC nervous system and neuropathies such as Alzheimer's and Parkinson's  
 XX CC diseases and Shy-drager syndrome, and mechanical and traumatic disorders,  
 XX CC such as spinal cord disorders, head trauma and stroke. The proteins may  
 XX CC also be used as a contraceptive and for treating coagulation disorders  
 XX CC such as haemophilias. The protein and nucleotide sequences with cadherin  
 XX CC activity are useful for treating cancer. Other uses for the protein  
 XX CC include for inhibiting the growth, infection or function of, or killing,  
 XX CC infectious agents such as bacteria, virus, fungi and other parasites, for  
 XX CC effecting bodily characteristics such as height, weight, hair colour,  
 XX CC effecting biorhythms or cardiac cycles or rhythms, effecting metabolism,  
 XX CC catabolism, anabolism, processing, utilization, storage or elimination of  
 XX CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors,  
 XX CC effecting behavioural characteristics, providing analgesic effects and  
 XX CC for treating hyperproliferative disorders such as psoriasis

XX SQ Sequence 113 AA;

Query Match 62.4%; Score 580; DB 3; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-63;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 70 MFVAVFLMTVTLVFNLFQHLHMLYMPVPLVLMINISATVLYITAFIACSAVDLT 129  
 Db 1 MFVAVFLMTVTLVFNLFQHLHMLYMPVPLVLMINISATVLYITAFIACSAVDLT 60  
 QY 130 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQAGGYA 182  
 Db 61 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSQAGGYA 113

RESULT 8  
 ABB90110  
 ID ABB90110 standard; protein; 113 AA.  
 XX AC ABB90110;  
 XX DT 24-MAY-2002 (first entry)  
 XX DE Human polypeptide SEQ ID NO 2486.  
 XX KW Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX OS Homo sapiens.  
 XX PN WO200190304-A2.  
 XX PD 29-NOV-2001.  
 XX PF 18-MAY-2001; 2001WO-US016450.  
 XX PR 19-MAY-2000; 2000US-0205515P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Birse CE, Rosen CA;  
 XX WPI; 2002-122018/16.  
 XX DR N-PSDB; ABL90519.  
 XX PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
 XX PT prevention of neural, immune system, muscular, reproductive,  
 XX PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
 XX PT disorders.  
 XX PS Claim 11; SEQ ID NO 2486; 2081pp + Sequence Listing; English.  
 XX CC The invention relates to novel genes (ABL99449-ABL90853) and proteins  
 XX CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating  
 XX CC medical conditions e.g. by protein or gene therapy. The genes are  
 XX CC isolated from a range of human tissues disclosed in the specification.  
 XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 XX CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 XX CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing  
 XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 XX CC infectious diseases such as viral, bacterial, fungal and parasitic  
 XX CC infections. Note: The sequence data for this patent did not form part of  
 XX CC the printed specification, but was obtained in electronic format directly  
 XX CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 62.4%; Score 580; DB 5; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-63;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MFVAVFLMLTVTLVFNLYLQLEHMKLVMPWPLVLMFNISATVLYITAFIACSAVDLT 129  
 Db 1 MFVAVFLMLTVTLVFNLYLQLEHMKLVMPWPLVLMFNISATVLYITAFIACSAVDLT 60

QY 130 SLRTRPYNQRAAASFFACLVMIAYGVSAFFSYQAMRGVGSNAATSQMAGGYA 182  
 Db 61 SLRTRPYNQRAAASFFACLVMIAYGVSAFFSYQAMRGVGSNAATSQMAGGYA 113

RESULT 9  
 AAY53643  
 ID AAY53643 standard; protein; 173 AA.  
 AC AAY53643;  
 DT 22-FEB-2000 (first entry)  
 DE A bone marrow secreted protein designated BMS6.  
 XX Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
 KW stem cell disorder; aplastic anaemia; bone differentiation;  
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
 KW bone fracture; cartilage damage; artificial joint.  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO9933979-A2.  
 XX  
 XX 08-JUL-1999.  
 XX  
 XX 18-DEC-1998; 98WO-US027008.  
 XX  
 XX 20-DEC-1997; 97US-0068958P.  
 PR 24-SEP-1998; 98US-0101603P.  
 PR 30-SEP-1998; 98US-0102540P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Lin H, Cao L;  
 XX  
 XX WPI; 2000-038344/03.  
 DR N-P8DB; AA236249.  
 XX  
 XX New isolated human polynucleotide and secreted proteins can induce  
 PT production of other cytokines in certain cell populations.  
 PT  
 XX  
 XX Claim 2; Page 119; 120pp; English.  
 PS  
 CC AAY53622-43 represent bone marrow secreted proteins of human bone marrow  
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
 CC cell differentiation activity (either inducing or inhibiting). They can  
 CC be used to support colony forming cells or factor-dependent cell lines,  
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
 CC deficiencies. In addition, they may be used to support the growth and  
 CC proliferation of erythroid progenitor cells, and to treat various  
 CC anaemias. They can have colony stimulating factor (CSF) activity and can  
 CC be used to support the growth and proliferation of myeloid cells such as  
 CC granulocytes, monocytes or macrophages, to prevent or treat myelo-  
 CC suppression, to support the growth and proliferation of megakaryocytes  
 CC and platelets, thereby allowing prevention or treatment of platelet  
 CC disorders such as thrombocytopenia, to support the growth and  
 CC proliferation of hematopoietic stem cells, either in place of or in

CC conjunction with platelet transfusions, to treat stem cell disorders,  
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
 CC repopulate the stem cell compartment after irradiation or chemotherapy.  
 CC They can be used for growth or differentiation of bone, cartilage,  
 CC tendon, ligament, or nerve tissue, as well as for wound healing and  
 CC tissue repair and replacement, and in the treatment of burns, incisions  
 CC and ulcers, to induce cartilage and/or bone growth in circumstances where  
 CC bone is not normally formed and thus have an application in healing bone  
 CC fractures and cartilage damage or defects, prophylactic use in fracture  
 CC reduction and also in the improved fixation of artificial joints  
 XX  
 XX Sequence 173 AA;  
 SQ

Query Match 34.9%; Score 325; DB 3; Length 173;  
 Best Local Similarity 43.8%; Pred. No. 1.1e-31;  
 Matches 71; Conservative 29; Mismatches 54; Indels 8; Gaps 2;

QY 8 VSTRSSPAQGAASVSALRDLGFSRLGALMLLQVLGLVWALIADTPHLYPAYG 67  
 Db 12 VTTASSFAENSTSSSFAYDREFLTPGLFVABIVLGLVWLTIACTEYRVPFAFG 71

QY 68 WMFVAVFLMLTVTLVFNLYLQLEHMKLVMPWPLVLMFNISATVLYITAFIACSAVD 127  
 Db 72 WMFVAVFLMLTVTLVFNLYLQLEHMKLVMPWPLVLMFNISATVLYITAFIACSAVD 126

QY 128 LTSL--RGTRPYNQRAAASFFACLVMIAYGVSAFFSYQAWR 166  
 Db 127 ASSVSPDRSHNFSNAASSFFAFVLTICVAGNTYFSFIAMR 168

RESULT 10  
 AAM25799  
 ID AAM25799 standard; protein; 173 AA.  
 AC AAM25799;  
 XX  
 XX 16-OCT-2001 (first entry)  
 DT  
 XX  
 XX Human protein sequence SEQ ID NO:1314.  
 DE  
 XX  
 XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
 KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;  
 KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;  
 KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200153455-A2.  
 PN  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 22-DEC-2000; 2000WO-US035017.  
 PF  
 XX 23-DEC-1999; 99US-00471275.  
 PR 21-JAN-2000; 2000US-00488725.  
 PR 25-APR-2000; 2000US-00552317.  
 XX  
 XX (HYPB-) HYSEQ INC.  
 PA  
 XX Tang YT, Liu C, Drmanac RT;  
 FI  
 XX WPI; 2001-457603/49.  
 DR

DR N-PSDB; AAH99740.  
XX Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.  
XX  
XX  
XX Claim 20; Page 273; 1217pp; English.  
XX  
XX AAH99166 to AAH99904 encode the human proteins given in AAH25225 to  
CC AAH25963. The proteins can have activities based on the tissues and cells  
CC they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antithrombotic; immunosuppressive; antibacterial; endocrine; cardiac;  
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;  
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders  
XX  
XX Sequence 173 AA;  
SQ  
Query Match 34.6%; Score 322; DB 4; Length 173;  
Best Local Similarity 42.4%; Pred. No. 2.7e-31;  
Matches 70; Conservative 30; Mismatches 57; Indels 8; Gaps 2;  
QY 5 PSKVRTRSSPAQGAASVSALRPLDGFVRSRLGALMLQLVLGLVWLIADTPYHLYP 64  
DB 9 PHAGTRKYSVPALSVHTSSSSSFAYDREPLRTLPGLIVAEIVLGLVWLIAGTEYFRVP 68  
QY 65 AYGVNMFVAVLWLVTVLNFNLQFLHMKLVMPWPLVLMFNISATVLYITAFIACSA 124  
DB 69 AFGVNMFAVAVVWLVTVLNFNLQFLHMKLVMPWPLVLMFNISATVLYITAFIACSA 123  
QY 125 AVDLTSL---RGRTPYNORAAASFFACLVMIAYGVSAFFSYQAWR 166  
DB 124 VVDASSVSPERDHNFNFWAASSFFAFLVTCIAGNTYFSFIAR 168  
RESULT 11  
ID AAW52117 standard; protein; 153 AA.  
XX  
XX AAW52117;  
XX  
XX 07-JUL-1998 (first entry)  
XX  
XX Human proteolipid (PLHu) protein.  
XX  
XX Human proteolipid; PLHu; exocytosis; membrane trafficking;  
KW rat plasmolipin; chemokine; inflammation.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Domain 20..40  
FT /note= "Transmembrane domain 1"  
FT Domain 50..72  
FT /note= "Transmembrane domain 2"  
FT Domain 84..108  
FT /note= "Transmembrane domain 3"  
FT Domain 127..147  
FT /note= "Transmembrane domain 4"  
XX

PN WO9804691-A1.  
XX  
XX 05-FEB-1998.  
PD  
XX 21-JUL-1997; 97WO-US012734.  
PF  
XX 26-JUL-1996; 96US-00695736.  
PR  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Au-Young J, Bandman O, Goli SK, Hillman JL;  
XX WPI; 1998-130683/12.  
XX N-PSDB; AAV17143.  
XX  
XX Human proteolipid PLHu - used to accelerate diagnosis and proper  
PT treatment of diseases and conditions associated with abnormal membrane  
PT trafficking.  
XX  
XX Claim 1; Fig 1A-1B; 53pp; English.  
PS  
XX The present sequence is of a human proteolipid (PLHu) protein which was  
CC expressed by PLHu cDNA of the current invention. A partial sequence of  
CC PLHu cDNA was initially isolated as incyte clone 640699 derived from a  
CC human breast cDNA library. Homology of PLHu protein to rat plasmolipin  
CC indicates its involvement in exocytosis. Exocytosis facilitated by PLHu  
CC may influence membrane trafficking within the cell and could affect the  
CC release of chemokines involved in cell migration, proteases which are  
CC active in inflammation or other similar activities involving endothelial  
CC cells, fibroblasts, etc. The invention also claims for antibodies against  
CC PLHu which can be used for e.g. in diagnostic tests to accelerate  
CC diagnosis and proper treatment of conditions associated with abnormal  
CC membrane trafficking  
XX  
XX Sequence 153 AA;  
SQ  
Query Match 33.0%; Score 307; DB 2; Length 153;  
Best Local Similarity 44.6%; Pred. No. 1.7e-29;  
Matches 66; Conservative 27; Mismatches 47; Indels 8; Gaps 2;  
QY 22 SVSALRPLDGFVRSRLGALMLQLVLGLVWLIADTPYHLYPAYGVNMFVAVFLMLVTI 81  
DB 6 SSSSFAYDREPLRTLPGLIVAEIVLGLVWLIAGTEYFRVFAFGVNMFAVAVFLVTV 65  
QY 82 VLFNLVLFQLHMKLVMPWPLVLMFNISATVLYITAFIACSAVDLTSL---RGRTPYN 138  
DB 66 FFLIYITMTYTRIPQVPTWTVGLCFNGSAFVLYLSA-----AVDASSVSPERDHNFN 120  
QY 139 QRAAASFFACLVMIAYGVSAFFSYQAWR 166  
DB 121 SWAASSFFAFLVNICYAGNTYFSFIAR 148  
RESULT 12  
ABP41095  
ID ABP41095 standard; protein; 132 AA.  
XX  
XX ABP41095;  
XX  
XX 22-AUG-2002 (first entry)  
XX  
XX Human ovarian antigen HSAVH65, SEQ ID NO:2227.  
XX  
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
KW inflammatory condition; immune disorder; blood disorder;  
KW cardiovascular disorder; respiratory disorder; neurological disorder;  
KW gastrointestinal disorder; urinary system disorder; drug screening;  
KW gene therapy; chromosome mapping; forensic analysis;  
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
KW antiinflammatory; gynaecological; reproductive.





ADA57177  
ID ADA57177 standard; protein; 100 AA.  
XX  
AC ADA57177;  
XX  
20-NOV-2003 (first entry)  
DT  
XX  
DE Human secreted protein #460.  
XX  
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
OS Homo sapiens.  
XX  
XX WO2002102994-A2.  
PN  
XX  
XX 27-DEC-2002.  
PD  
XX  
XX 19-MAR-2002; 2002WO-US008278.  
PF  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR  
XX 19-JUL-2001; 2001US-0306171P.  
PR  
XX 13-NOV-2001; 2001US-0331287P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2003-167512/16.  
XX N-PSDB; ADA56281.  
DR  
XX  
XX New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX  
XX Claim 13; SEQ ID NO 1367; 1754pp; English.  
PS  
XX  
XX The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at

ftp.wipo.int/pub/published\_pct\_sequences.  
CC  
XX Sequence 100 AA;  
SQ  
Query Match 20.5%; Score 191; DB 6; Length 100;  
Best Local Similarity 41.0%; Pred. No. 2.3e-15;  
Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;  
QY 70 MFVAVFVWLVTVLVFNLYLFLQHNKLYWVPLVLMFNISATVLYITAFIACSAADLT 129  
DB 1 MFVAVFVWLVTVLVFNLYLFLQHNKLYWVPLVLMFNISATVLYITAFIACSAADLT 129  
QY 130 SL---RGRTPYNQRAAASFFACLVMIAYGVSAFFSYQAWR 166  
DB 56 SVSEKSHNFNSWAASSFFAFLVITCYAGNTYFSEFXAWR 95  
RESULT 15  
ADA41044  
ID ADA41044 standard; protein; 100 AA.  
XX  
AC ADA41044;  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX  
XX Human secreted protein.  
DE  
XX  
XX Human; secreted protein; cancer; hyperproliferative disorder;  
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;  
KW anaemia; allergic reaction; asthma; cardiovascular disorder;  
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;  
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;  
KW vulnery; cardiant; gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2002102993-A2.  
PN  
XX  
XX 27-DEC-2002.  
PD  
XX  
XX 19-MAR-2002; 2002WO-US008123.  
PF  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR  
XX 19-JUL-2001; 2001US-0306171P.  
PR  
XX 13-NOV-2001; 2001US-0331287P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2003-175238/17.  
DR  
XX  
XX New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing,  
PT preventing or treating cancer or other hyperproliferative disorder,  
PT asthma, allergies or AIDS.  
XX  
XX Claim 1; SEQ ID NO 1426; 3205pp; English.  
PS  
XX  
XX The invention relates to novel genes ADA39629-ADA40565 and proteins  
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,  
CC treating or ameliorating medical conditions e.g. by protein or gene  
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their  
CC fragments, and agonists or antagonists that bind to the polypeptide are  
CC useful for preparing a diagnostic or pharmaceutical composition for  
CC diagnosing or treating cancer or other hyperproliferative disorder. The  
CC polypeptides and nucleic acid molecules are also useful for detecting,  
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer  
CC or other hyperproliferative disorders including neoplasms, autoimmune  
CC disorders (e.g. diabetes, rheumatoid arthritis,  
CC erythematous, multiple sclerosis, autoimmune thyroiditis or haemolytic  
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,  
CC thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory  
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.  
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders  
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,  
CC fungal or viral infections including HIV/AIDS), or wound healing and  
CC disorders of epithelial cell proliferation. The nucleic acids are also  
CC useful for chromosome identification, radiation hybrid mapping or long-  
CC range restriction mapping, as molecular weight markers, or as  
CC hybridization or diagnostic probes. The polypeptides and antibodies are  
CC useful for providing immunological probes for differential identification  
CC of the tissues immunohistochemistry assays. Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 100 AA;

Query Match 20.5%; Score 191; DB 6; Length 100;  
Best Local Similarity 41.0%; Pred. No. 2.3e-15;  
Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;  
Qy 70 MFVAVFLWLTIVLFLNLYLPQLHMKLYMPEPLVLMFNISATVLYITAFIACSAVDLT 129  
Db 1 MFVAVFYWLTVFLIIITWTYTRIPQVPTTVCFCNGSAFVLYLSA-----AVVDAS 55  
Qy 130 SL---RGTRPYNQRAAASFACLVMIAYGVSAFFSYQAWR 166  
Db 56 SVSPKDSHNFNFWAASSFFAFLVTCYAGNTYFSFXAWR 95

Search completed: December 1, 2004, 15:43:41  
Job time : 159 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 15:29:28 ; Search time 40 Seconds  
(without alignments)  
301.747 Million cell updates/sec

Title: US-09-602-597A-4  
Perfect score: 930  
Sequence: 1 NAEFSPKSTRTSSPAQGAEE.....QAKRGVGSNAATSQMAGYA 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/prodata/1/aaa/5A-COMB.pep: \*  
2: /cgn2\_6/prodata/1/aaa/5B-COMB.pep: \*  
3: /cgn2\_6/prodata/1/aaa/6A-COMB.pep: \*  
4: /cgn2\_6/prodata/1/aaa/6B-COMB.pep: \*  
5: /cgn2\_6/prodata/1/aaa/PCrUS-COMB.pep: \*  
6: /cgn2\_6/prodata/1/aaa/backfiles1.pep: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	79.7	157	2	US-08-695-736-3
2	307	33.0	153	2	US-08-695-736-1
3	153	16.5	153	2	US-08-695-736-4
4	148.5	16.0	148	4	US-09-702-705-338
5	148.5	16.0	148	4	US-09-736-457-338
6	148.5	16.0	148	4	US-09-614-124B-338
7	148.5	16.0	148	4	US-09-671-325-338
8	148.5	16.0	148	4	US-09-589-184-338
9	148.5	16.0	148	4	US-09-558-824-338
10	127.5	13.7	289	4	US-09-520-781-28
11	91	9.8	421	4	US-09-198-452A-932
12	88.5	9.5	220	4	US-09-328-714A-4
13	88	9.5	296	4	US-09-107-532A-6356
14	87	9.4	448	4	US-09-328-352-5694
15	86.5	9.3	211	4	US-09-252-991A-23822
16	86.5	9.3	289	3	US-09-724-864-47
17	86.5	9.3	400	1	US-07-916-901-6
18	86.5	9.3	400	1	US-07-783-602C-1
19	86.5	9.3	400	1	US-08-351-473B-4
20	85	9.1	446	4	US-09-352-991A-22844
21	84.5	9.1	378	4	US-09-560-761-18
22	82.5	8.9	224	4	US-09-270-767-43554
23	82.5	8.9	279	4	US-09-248-756A-16033
24	82	8.8	395	4	US-09-560-761-22
25	81.5	8.8	388	1	US-08-087-772A-2
26	81.5	8.8	400	1	US-08-351-473B-5
27	81.5	8.8	400	3	US-08-450-962-4

28	81.5	8.8	400	3	US-08-450-962-6	Sequence 6, Appli
29	81.5	8.8	400	4	US-08-848-631-4	Sequence 4, Appli
30	81.5	8.8	400	4	US-08-848-631-6	Sequence 6, Appli
31	81	8.7	255	4	US-09-549-848B-24	Sequence 24, Appli
32	81	8.7	257	4	US-09-560-761-12	Sequence 12, Appli
33	81	8.7	304	3	US-09-134-001C-4518	Sequence 4518, Ap
34	81	8.7	382	4	US-09-560-761-14	Sequence 14, Appli
35	80.5	8.7	262	3	US-09-134-001C-3932	Sequence 3932, Ap
36	80.5	8.7	430	4	US-09-489-039A-10587	Sequence 10587, A
37	80	8.6	597	4	US-09-252-991A-32657	Sequence 32657, A
38	79	8.5	373	4	US-09-107-532A-6084	Sequence 6084, Ap
39	78.5	8.4	383	4	US-09-560-761-28	Sequence 28, Appli
40	78.5	8.4	408	3	US-09-134-001C-3410	Sequence 40, Appli
41	78	8.4	263	4	US-10-000-489-40	Sequence 11233, A
42	78	8.4	957	4	US-09-489-039A-11233	Sequence 7902, Ap
43	77.5	8.3	255	4	US-09-328-352-7902	Sequence 31786, A
44	77.5	8.3	344	4	US-09-252-991A-31786	Sequence 4426, Ap
45	77.5	8.3	345	4	US-09-107-532A-4426	

## ALIGNMENTS

RESULT 1  
US-08-695-736-3  
; Sequence 3, Application US/09695736  
; Patent No. 5843714  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,736  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/POCKET NUMBER: PF-0108 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1346732  
US-08-695-736-3

Query Match 79.7%; Score 741; DB 2; Length 157;  
Best Local Similarity 87.9%; Pred No. 4, 9e-72;  
Matches 138; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 26 LRPD:GFVRSRGALMLLQLVLGLLWALADTFPHLYPAYGWNFVAVFLWLVTLVFN 85

Db 1 MRPDGVRVSALGVALLQLVLGLVWALVADTPYHLYPAYGWMFVAVFLMLVTVFFI 60  
QY 86 LYLPLQHLKLMVWPLVLMFNISATVLYITAFIACSAVDLTSLGTRPNQRAAASF 145  
Db 61 IYLPQHLKLMVWPLVLLVFFVFAATVLYITAFVACAAVDLTSLGSRPNQRAAASF 120  
QY 146 FACLVMIAYGVSFFSQAVRGVGSNAATSQMAGGYA 182  
Db 121 FACLVMIAYGVSFFSQAVRGVGSNAATSQMAGGYS 157

RESULT 2  
US-08-695-736-1  
; Sequence 1, Application US/08695736  
; Patent No. 5843714  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,736  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0108 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT03  
; CLONE: 640699

US-08-695-736-1  
Query Match 33.0%; Score 307; DB 2; Length 153;  
Best Local Similarity 44.6%; Pred. No. 2.2e-25;  
Matches 66; Conservative 27; Mismatches 47; Indels 8; Gaps 2;  
QY 22 SVSALRPDLGFRVSRGLGALMLQLVLGLVWALVADTPYHLYPAYGWMFVAVFLMLVTV 81  
Db 6 SSSSFAYDREFLTLPGFLVIAEVLGLVWALVADTPYHLYPAYGWMFVAVFLMLVTV 65  
QY 82 VLFLNLYLPQLHMKLMVWPLVLMFNISATVLYITAFIACSAVDLTSLGTRPNQRAAASF 138  
Db 66 FELIYITWTYTRIPQVPTTTLGCLFNGSAFVLYLSA-----AVVDASSVSPDRSDNFN 120  
QY 139 QRAAASFFACLVMIAYGVSFFSQAVRGVGSNAATSQMAGGYA 166  
Db 121 SWAASSFFAFVLCVAGNYTFSPIAWR 148

RESULT 3  
US-08-695-736-4  
; Sequence 4, Application US/08695736  
; Patent No. 5843714  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEOLIPID  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/695,736  
; FILING DATE: Filed Herewith  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0108 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 153 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 126719  
US-08-695-736-4

Query Match 16.5%; Score 153; DB 2; Length 153;  
Best Local Similarity 30.2%; Pred. No. 7.8e-09;  
Matches 45; Conservative 25; Mismatches 61; Indels 18; Gaps 6;  
QY 22 SVSALRPDLGFRVSRGLGALMLQLVLGLVWALVADTPYHLYPAYGWMFVAVFLMLV 79  
Db 17 SVFTTLPLD-----LFIFFIFGGLVWLVASSLVFWPL--VQGWVWFVSVECFVA 65  
QY 80 TIVFLNLYLPQLHMKLMVWPLVLMFNISATVLYITAFIACSAVDLTSLGTRPNQRAAASF 137  
Db 66 TTVLILYIIGAHGG--ETSWVLDAAYHCTAALFVLSASV-LEALATITMQDGFYRHY 122  
QY 138 NQRAAASFFACLVMIAYGVSFFSQAVRGVGSNAATSQMAGGYA 166  
Db 123 HENIAAVFSYIATLLYVWVHAFSLIRWK 151

RESULT 4  
US-09-702-705-338  
; Sequence 338, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom

```

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-338

Query Match 16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLP-AYGWMFVAVFLWLVTVLVFNLYLFQLHMKLYM 97
Db 24 AFPLPELIFGLVWMTVAAT-HIVYPLLQGWVYVSLTSLMFLSLYLFGLFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNORAAASFFACLVMIAYGV 156
Db 81 ESWRVLDLSYHGTTGILYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 5
US-09-736-457-338
; Sequence 338, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-338

Query Match 16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLP-AYGWMFVAVFLWLVTVLVFNLYLFQLHMKLYM 97
Db 24 AFPLPELIFGLVWMTVAAT-HIVYPLLQGWVYVSLTSLMFLSLYLFGLFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNORAAASFFACLVMIAYGV 156
Db 81 ESWRVLDLSYHGTTGILYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

US-09-614-124B-338
; Sequence 338, Application US/09614124B
; Patent No. 8630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-338

Query Match 16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALIADTPHYLP-AYGWMFVAVFLWLVTVLVFNLYLFQLHMKLYM 97
Db 24 AFPLPELIFGLVWMTVAAT-HIVYPLLQGWVYVSLTSLMFLSLYLFGLFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNORAAASFFACLVMIAYGV 156
Db 81 ESWRVLDLSYHGTTGILYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

US-09-671-325-338
; Sequence 338, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-09-671-325-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALLIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQLHMKLYM 97
Db 24 AFFPELIFGLFWMTVAAT-HIVYPLQGWVMYVSLTSLIMFLLSYLFQFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 8
US-09-589-184-338
; Sequence 338, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALLIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQLHMKLYM 97
Db 24 AFFPELIFGLFWMTVAAT-HIVYPLQGWVMYVSLTSLIMFLLSYLFQFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 9
US-09-658-824-338
; Sequence 338, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; ORGANISM: Homo sapiens
US-09-658-824-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALLIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQLHMKLYM 97
Db 24 AFFPELIFGLFWMTVAAT-HIVYPLQGWVMYVSLTSLIMFLLSYLFQFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 10
US-09-520-781-28
; Sequence 28, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-28

Query Match      13.7%; Score 127.5; DB 4; Length 299;
Best Local Similarity 25.7%; Pred. No. 9.9e-06;
Matches 33; Conservative 25; Mismatches 66; Indels 19; Gaps 3;

QY 37 LGALMLQLVLGLLWALLIADTPHYLYPAYGWMFVAVFLWLVTLVFNLYL-----FQ 90
Db 13 LGLRLQLVSTCTVAFSLVASVGAWTGSNGNSMTWCFCFSVTLIIILIVELCGLQARFP 72
QY 91 LHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLTSLRGTRPNQRAAASFFACL 150
Db 73 LSWRNPITTFACVAALFCLASIIYPTTV-----OFLSHGRSRDHAIATPFSCIA 124
QY 151 MIAYGVSAFFSYQAWRGVGSNAATSQMA 178
Db 125 CVAYATEV-----AWTRARPGEITGMA 147

RESULT 11
US-09-198-452A-932
```

```

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-658-824-338

Query Match      16.0%; Score 148.5; DB 4; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.3e-08;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVLGLLWALLIADTPHYLYP-AYGWMFVAVFLWLVTLVFNLYLFQLHMKLYM 97
Db 24 AFFPELIFGLFWMTVAAT-HIVYPLQGWVMYVSLTSLIMFLLSYLFQFYKR--F 80
QY 98 VPWPLVLMFNISATVLYIT-AFIACSAAVDLTSLRGTRPNQRAAASFFACLVMYAGV 156
Db 81 ESMRVLDSLYHGTTGLYMSAAVLQVHATIVSEKLLDPRIYYINSAASFFAFIATLLYL 140
QY 157 SAFPSY 162
Db 141 HAFSIY 146

RESULT 10
US-09-520-781-28
; Sequence 28, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-520-781-28

Query Match      13.7%; Score 127.5; DB 4; Length 299;
Best Local Similarity 25.7%; Pred. No. 9.9e-06;
Matches 33; Conservative 25; Mismatches 66; Indels 19; Gaps 3;

QY 37 LGALMLQLVLGLLWALLIADTPHYLYPAYGWMFVAVFLWLVTLVFNLYL-----FQ 90
Db 13 LGLRLQLVSTCTVAFSLVASVGAWTGSNGNSMTWCFCFSVTLIIILIVELCGLQARFP 72
QY 91 LHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLTSLRGTRPNQRAAASFFACL 150
Db 73 LSWRNPITTFACVAALFCLASIIYPTTV-----OFLSHGRSRDHAIATPFSCIA 124
QY 151 MIAYGVSAFFSYQAWRGVGSNAATSQMA 178
Db 125 CVAYATEV-----AWTRARPGEITGMA 147

RESULT 11
US-09-198-452A-932
```

; Sequence 932, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Grifais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 932  
; LENGTH: 421  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-932

Query Match 9.8%; Score 91; DB 4; Length 421;  
Best Local Similarity 24.0%; Pred. No. 0.13;  
Matches 35; Conservative 24; Mismatches 49; Indels 38; Gaps 5;

QY 23 VSALRPDLGVSRLGAL-----MLQLVLGLLVKALADTPHYLPAYGVMFVAVFL 76  
DB 71 ISSMDPTAMLVSSKGLINKIMQLRHPALGWNVFFICAYDYHLFKRWAVLY--PFM 128  
QY 77 WLVTIVFLNLYLFQLHMKLYMPW-----PLVLMIFNISATVLYITAFACSA 125  
DB 129 ICALVGLFFVPSONVHRWYRIFPHMSVQPSYKGLVIV-----MLSYILES 179  
QY 126 VLTSLRGTRPNQRAAASFFACLVM 151  
DB 180 ADITS-----KTTAFLACLTV 195

RESULT 12  
US-09-328-714A-4  
; Sequence 4, Application US/09328714A  
; Patent No. 6500940  
; GENERAL INFORMATION:  
; APPLICANT: The Salk Institute for Biological Sciences  
; APPLICANT: Inder M. Verma  
; APPLICANT: Mark Schmitt  
; APPLICANT: Nikunj V. Somia  
; TITLE OF INVENTION: LIFE GUARD (LFG) POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS OF USE THEREOF  
; FILE REFERENCE: SALKINS.016A  
; CURRENT APPLICATION NUMBER: US/09/328,714A  
; CURRENT FILING DATE: 1999-06-09  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: C. elegans  
US-09-328-714A-4

Query Match 9.5%; Score 88.5; DB 4; Length 220;  
Best Local Similarity 17.7%; Pred. No. 0.11;  
Matches 22; Conservative 27; Mismatches 54; Indels 21; Gaps 2;

QY 68 WNFVAVFLMLVTLVLF-----NLVLFQLHMKLYMPVPLVLMIFNISATVLY 115  
DB 44 WYFIALIVFLVIALSCGNLRQFPVNIILLTIFLSAAVMTFVTACYNVQSVLIC 103  
QY 116 ITAFIACSAVDLTSRGTFRPNQRAAASFFACLVMYGVSAF-----FSQAWR 166  
DB 104 LCITTCVSGSVIIFSMKTSDLTSKMGIAFMLSMVLFSFGIFALIFTLAPNMQFLSVYS 163  
QY 167 GVGS 170  
DB 164 GLAA 167

RESULT 13  
US-09-107-532A-6356  
; Sequence 6356, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6356:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 296 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...296  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6356:  
US-09-107-532A-6356

Query Match 9.5%; Score 88; DB 4; Length 296;  
Best Local Similarity 22.9%; Pred. No. 0.17;  
Matches 38; Conservative 26; Mismatches 50; Indels 50; Gaps 7;

QY 46 VLGLLVWALIAADTPYHL--YPAYGVMFVAVFLMLVTLV-----FNL 86  
DB 21 IVGLVVLALVGLFFPYLGMQAKVWALFSLFLLTLLSSATVWSPNQKVLFFGQ 80  
QY 87 YLFQLHMKLYMPVPLV-----LMIFNISATVLYITAFIACSAVDLTSRGTFRPNQR 140  
DB 81 YLGTIRENGFFLTPLAQKQMTVSLKVRNFNSVLKVN-----BLDG-----NP 127  
QY 141 AAASF-----FACLVMTAYGVSFAFFSQAAMRGVGSNAATSQMAGGY 181  
DB 128 AVVFKVVDTKALFDVAY-----YQDFVEIQSETAIRHIAQY 166

RESULT 14  
US-09-328-352-5694  
; Sequence 5694, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5694  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5694

Query Match 9.4%; Score 87; DB 4; Length 448;  
Best Local Similarity 22.2%; Pred. No. 0.37; Mismatches 27; Indels 58; Gaps 7;  
Matches 43; Conservative 27; Mismatches 58; Indels 56; Gaps 7;  
QY 27 RPDL-----GFRSRLGALM-----LLQLVLGLLWALIA-----DTPYH----- 61  
DQ 69 RPDLGGGYNVAREGFDLIGCSAWYLCCTTIGIVGVYVIAFSGVGMETDSKDHVIFG 128  
QY 62 ----LYPAYGWMFVAFVLMV-----TIVLFNLYLF 89  
DQ 129 EGNLTLYSLIGSSIFWFLVHVLVSRGIXEAAIYNLLATIAKIIIMVVFIFFTFIARFDLF 188  
QY 90 QLHMKLYWVWPLVLMIFNISATVLYITAFIACSAVDLTSLRGTRPYNORA-----A 142  
DQ 189 KLNLDLSLKVPLWQVKDMLTLV--FTGIEGAVLSSRAKNRHDIGKATILGVLLA 246  
QY 143 ASPFACLVMIAYGV 156  
DQ 247 LSFYVMTVLAYGV 260

RESULT 15  
US-09-252-991A-23822  
; Sequence 23822, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23822  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23822

Query Match 9.3%; Score 86.5; DB 4; Length 211;  
Best Local Similarity 32.8%; Pred. No. 0.16;  
Matches 38; Conservative 15; Mismatches 36; Indels 27; Gaps 5;  
QY 20 EASVSALRPDLGFV--RSLGALMLLQLVLGLLWALIAADTPYHLYPAYGWMFVAV-- 74  
DQ 33 QAWIFALGPDGKTYLVDRLGLGALVLLLTLAN-----TP--LQKLSGWPGWIAVER 82  
QY 75 --FLWLVTVLFNLYLF-----QLHMKLYWVWPLVLMIFNISATVLYITA 118  
DQ 83 QLGLWCFTYVLLHLSAYCVFILGDLWDGQLGIELSKRPIIIVGMLGFCFLAITS 138

Search completed: December 1, 2004, 15:47:42  
Job time : 42 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 15:47:12 ; Search time 145 Seconds  
(without alignments)  
447.623 Million cell updates/sec

Title: US-09-602-597A-4  
Perfect score: 930  
Sequence: 1 MAEPFSKVTSTSSPAQAE.....QAWRGVGSNAATSQMAGYA 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 35623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	930	100.0	216	14	US-10-263-230A-4
2	625	67.2	125	15	US-10-264-237-2440
3	580	62.4	113	15	US-10-264-237-2486
4	325	34.9	173	9	US-09-765-205-44
5	322	34.6	173	15	US-10-296-115-1314
6	283	30.4	132	15	US-10-264-048-2227
7	191	20.5	100	15	US-10-553-593-194
8	191	20.5	101	10	US-09-397-945-194
9	162	17.4	176	11	US-09-833-245-1314
10	162	17.4	176	14	US-10-176-847-20
11	162	17.4	176	14	US-10-097-340-282
12	162	17.4	215	15	US-10-264-049-2873
13	153	16.5	153	14	US-10-257-021-74

Query Match	100.0%	Score	930	DB	14	Length	216
Best Local Similarity	100.0%	Pred. No.	5.4e-88				
Matches	182	Conservative	0	Mismatches	0	Indels	0
Gaps	0						

  

QY	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLVWALIADTPY	60
DB	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLVWALIADTPY	60
QY	61	HLYPAGWVMFVAVFLMLVTIVLFLNLYLQFQHMKLYMVPWPLVLMIFNISATVITAFI	120
DB	61	HLYPAGWVMFVAVFLMLVTIVLFLNLYLQFQHMKLYMVPWPLVLMIFNISATVITAFI	120
QY	121	ACSAAVDITSLRGTPYNNQRAAASFPACLVMIAYGVSAFFSVQAWRGVGSNAATSQMAGG	180
DB	121	ACSAAVDITSLRGTPYNNQRAAASFPACLVMIAYGVSAFFSVQAWRGVGSNAATSQMAGG	180

## ALIGNMENTS

RESULT 1  
US-10-263-230A-4  
; Sequence 4, Application US/10263230A  
; Publication No. US20030152963A1  
; GENERAL INFORMATION:  
; APPLICANT: Duhi, David  
; TITLE OF INVENTION: HUMAN CHROMOSOME 15 AND 16 BARDET-BIEDL  
; TITLE OF INVENTION: SYNDROME POLYNUCLEOTIDES AND POLYPEPTIDES AND METHODS OF USE  
; FILE REFERENCE: 59516-243/PP-1568.002  
; CURRENT APPLICATION NUMBER: US/10/263.230A  
; CURRENT FILING DATE: 2002-10-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 216  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-263-230A-4

Query Match	100.0%	Score	930	DB	14	Length	216
Best Local Similarity	100.0%	Pred. No.	5.4e-88				
Matches	182	Conservative	0	Mismatches	0	Indels	0
Gaps	0						

  

QY	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLVWALIADTPY	60
DB	1	MAEPFSKVTSTSSPAQAEASVSALRDLGFSVSRGALMLQLVLGLVWALIADTPY	60
QY	61	HLYPAGWVMFVAVFLMLVTIVLFLNLYLQFQHMKLYMVPWPLVLMIFNISATVITAFI	120
DB	61	HLYPAGWVMFVAVFLMLVTIVLFLNLYLQFQHMKLYMVPWPLVLMIFNISATVITAFI	120
QY	121	ACSAAVDITSLRGTPYNNQRAAASFPACLVMIAYGVSAFFSVQAWRGVGSNAATSQMAGG	180
DB	121	ACSAAVDITSLRGTPYNNQRAAASFPACLVMIAYGVSAFFSVQAWRGVGSNAATSQMAGG	180

QY 181 YA 182  
||  
Db 181 YA 182

## RESULT 2

US-10-264-237-2440  
; Sequence 2440, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P4131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: Patent in Ver. 3.1  
; SEQ ID NO 2440  
; LENGTH: 125  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (118)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-2440

Query Match 67.2%; Score 625; DB 15; Length 125;  
Best Local Similarity 97.6%; Pred. No. 1e-56; Indels 0; Gaps 0;  
Matches 122; Conservative 0; Mismatches 3;

QY 1 MAEPKSVKSTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPY 60  
|||  
Db 1 MAEPKSVKSTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPY 60  
  
QY 61 HLPAYGWVFMVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFI 120  
|||  
Db 61 HLPAYGWVFMVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFI 120  
  
QY 121 ACSAA 125  
|||  
Db 121 GCSAA 125

## RESULT 3

US-10-264-237-2486  
; Sequence 2486, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P4131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: Patent in Ver. 3.1  
; SEQ ID NO 2486  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-237-2486

Query Match 62.4%; Score 580; DB 15; Length 113;  
Best Local Similarity 100.0%; Pred. No. 4.2e-52;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLT 129  
|||  
Db 1 MFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVDLT 60  
  
QY 130 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSONAGGYA 182  
|||  
Db 61 SLRGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWRGVGSNAATSONAGGYA 113

## RESULT 4

US-09-765-205-44  
; Sequence 44, Application US/09765205  
; Patent No. US20020034800A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Li  
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
; FILE REFERENCE: 1458.004/200130.449  
; CURRENT APPLICATION NUMBER: US/09/765,205  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US/09/212,440  
; PRIOR FILING DATE: 1998-12-16  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 173  
; TYPE: PRT  
; ORGANISM: human  
US-09-765-205-44

Query Match 34.9%; Score 325; DB 9; Length 173;  
Best Local Similarity 43.8%; Pred. No. 1.7e-25;  
Matches 71; Conservative 29; Mismatches 54; Indels 8; Gaps 2;

QY 8 VSTRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPHYLYPAG 67  
|||  
Db 12 VTTASSFAENFSTSSSFPAYDREFLRPLGFLIVAIIVLGLLWTLIAGTEYFRVPAFG 71  
  
QY 68 WMFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVD 127  
|||  
Db 72 WMFVAVFLMLVTLVFNLYLQHLHMKLYMVPWPLVLMFNISATVLYITAFIACSAAVD 126  
  
QY 128 LTSL---RGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWR 166  
|||  
Db 127 ASSVSPEDSHNFNSWAASFFAFVLTICAGNTYFFSFIAR 168

## RESULT 5

US-10-296-115-1314  
; Sequence 1314, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 1314  
; LENGTH: 173  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-296-115-1314

Query Match 34.6%; Score 322; DB 15; Length 173;  
Best Local Similarity 42.4%; Pred. No. 3.4e-25;  
Matches 70; Conservative 30; Mismatches 57; Indels 8; Gaps 2;

QY 5 PSKVSRTSSPAQGAASVSALRPDLGFRVSRIGALMLQLVLGLLVWALIADTPHYLYP 64

Db 9 PNACTRYKVSYPALSHVHTSSSFAYDREFLTLFGFLVAEIVGLLWTLIAGTEYRVP 68  
QY 55 AYGHWMFVAFVFLVTLVFLNLYLQFLHMKLYMVPWPLVMFNISATVLYITAFIACA 124  
Db 69 AFGWMFVAFVFLVTLVFLNLYLQFLHMKLYMVPWPLVMFNISATVLYITAFIACA 123  
QY 125 AVDLTSL---RGTRPNQRAAASFFACLVMIAYGVSAFTSYQAWR 166  
Db 124 VVDASSVSPEDSHNFNSWAASSFFAFVLTICVAGNTYFSFIAR 168

## RESULT 6

US-10-264-049-2227  
; Sequence 2227, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P4133P1  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: Patent in Ver. 3.1  
; SEQ ID NO 2227  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-049-2227

Query Match 30.4%; Score 283; DB 15; Length 132;

Best Local Similarity 46.0%; Pred. No. 2.7e-21;

Matches 58; Conservative 23; Mismatches 37; Indels 8; Gaps 2;

QY 44 QLVGLLWVLIADTPYHLYPAYGWVFAVFLVTLVFLNLYLQFLHMKLYMVPWPLV 103  
Db 7 EIVGLLWVLIAGTEYRVPAGWVFAVFLVTLVFLNLYLQFLHMKLYMVPWPLV 66  
QY 104 LMIFNISATVLYITAFIACAADLTSL---RGTRPNQRAAASFFACLVMIAYGVSAFF 160  
Db 67 GLCFNGSAFVLYLSA-----AVVDASSVSPKDSHNFNSWAASSFFAFVLTICVAGNTYF 121  
QY 161 SYQAWR 166  
Db 122 SFIAR 127

## RESULT 7

US-10-653-595-194  
; Sequence 194, Application US/10653595  
; Publication No. US20040048304A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 95 Human secreted proteins  
; FILE REFERENCE: P2027P1C1  
; CURRENT APPLICATION NUMBER: US/10/653,595  
; CURRENT FILING DATE: 2003-09-03  
; PRIOR APPLICATION NUMBER: US 09/397945  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: PCT/US99/05804  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,566  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,576  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,573  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,574

; PRIOR APPLICATION NUMBER: 60/078,579  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/080,314  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080,312  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/078,578  
; PRIOR FILING DATE: 1998-03-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 194  
; LENGTH: 100  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (92)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (96)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-653-595-194

Query Match 20.5%; Score 191; DB 15; Length 100;

Best Local Similarity 41.0%; Pred. No. 6.5e-12;

Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;

QY 70 MFVAVFLVTLVFLNLYLQFLHMKLYMVPWPLVMFNISATVLYITAFIACAADLT 129  
Db 1 MFVAVFLVTLVFLNLYLQFLHMKLYMVPWPLVMFNISATVLYITAFIACAADLT 55  
QY 130 SL---RGTRPNQRAAASFFACLVMIAYGVSAFFSYQAWR 166  
Db 56 SVSPKDSHNFNSWAASSFFAFVLTICVAGNTYFSFIAR 95

## RESULT 8

US-09-397-945-194  
; Sequence 194, Application US/09397945  
; Publication No. US200300065139A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc. et al.  
; TITLE OF INVENTION: 95 Human secreted proteins  
; FILE REFERENCE: P2027P1  
; CURRENT APPLICATION NUMBER: US/09/397,945  
; CURRENT FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: PCT/US99/05804  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,566  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,576  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,573  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,574  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,579  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/080,314  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080,312  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/078,578  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,581  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,577  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,563  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/080,313

; PRIOR FILING DATE: 1998-04-01  
 ; NUMBER OF SEQ ID NOS: 470  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 194  
 ; LENGTH: 101  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (92)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (96)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (101)  
 ; OTHER INFORMATION: Xaa equals stop translation  
 ; US-09-397-945-194

Query Match 20.5%; Score 191; DB 10; Length 101;  
 Best Local Similarity 41.0%; Pred. No. 6.6e-12;  
 Matches 41; Conservative 20; Mismatches 31; Indels 8; Gaps 2;  
 QY 70 MFVAVFLWLVTVLNLFLQLHMKLVMPPLVLMFNISATVLYITAFIACSAVDLT 129  
 DB 1 MFVAVFWLVTVLNLFLQLHMKLVMPPLVLMFNISATVLYITAFIACSAVDLT 129  
 QY 130 SL--RGTTPYQNRASAFACLVMIAYGVSAFFSYQAWR 166  
 DB 56 SVSPKDSHNFNGSWAASSPFAFLVTCYAGNTVFSFXWR 95

## RESULT 9

US-09-833-245-1314  
 ; Sequence 1314, Application US/09833245  
 ; Publication No. US20040010134A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Albumin Fusion Proteins  
 ; FILE REFERENCE: PF546PCT  
 ; CURRENT APPLICATION NUMBER: US/09/833,245  
 ; PRIOR FILING DATE: 2001-04-12  
 ; PRIOR APPLICATION NUMBER: 60/229,358  
 ; PRIOR FILING DATE: 2000-04-12  
 ; PRIOR APPLICATION NUMBER: 60/256,931  
 ; PRIOR FILING DATE: 2000-12-21  
 ; PRIOR APPLICATION NUMBER: 60/199,384  
 ; PRIOR FILING DATE: 2000-04-25  
 ; NUMBER OF SEQ ID NOS: 2267  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1314  
 ; LENGTH: 176  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-833-245-1314

Query Match 17.4%; Score 162; DB 11; Length 176;  
 Best Local Similarity 28.7%; Pred. No. 1.2e-08;  
 Matches 43; Conservative 30; Mismatches 63; Indels 14; Gaps 4;  
 QY 28 PDLGFRSLGALMLQLVLGLLVWALIADTPYHLYPAGVWVAVFLWLVTVLNLFL 87  
 DB 29 PDI--LRTYSGAFVCLLEIFGLGLVILVASSNVPLPLQGVWVSVTAFFSLLFLGMF 86  
 QY 88 LPQLHMKLVMPPLVLMFNISATVLYITAFIACSAVDLT-----TSLEG-----TRP 136  
 DB 87 LSGWVAQI--DANWNFDFAYHFTVFYFGAFLEAATSLHDLHCNTTITGQPLLSNQ 145  
 QY 137 YNQRASAFACLVMIAYGVSAFFSYQAWR 166  
 DB 146 YNINVAASIFAFMTTACVGCGLGLALRRWR 175

RESULT 10  
 US-10-176-847-20  
 ; Sequence 20, Application US/10176847  
 ; Publication No. US20030068636A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Veiby, Pette Ole  
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR  
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST  
 ; TUMORS  
 ; FILE REFERENCE: MRI-039  
 ; CURRENT APPLICATION NUMBER: US/10/176,847  
 ; CURRENT FILING DATE: 2002-06-21  
 ; NUMBER OF SEQ ID NOS: 112  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 20  
 ; LENGTH: 176  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-176-847-20

Query Match 17.4%; Score 162; DB 14; Length 176;  
 Best Local Similarity 28.7%; Pred. No. 1.2e-08;  
 Matches 43; Conservative 30; Mismatches 63; Indels 14; Gaps 4;  
 QY 28 PDLGFRSLGALMLQLVLGLLVWALIADTPYHLYPAGVWVAVFLWLVTVLNLFL 87  
 DB 29 PDI--LRTYSGAFVCLLEIFGLGLVILVASSNVPLPLQGVWVSVTAFFSLLFLGMF 86  
 QY 88 LPQLHMKLVMPPLVLMFNISATVLYITAFIACSAVDLT-----TSLEG-----TRP 136  
 DB 87 LSGWVAQI--DANWNFDFAYHFTVFYFGAFLEAATSLHDLHCNTTITGQPLLSNQ 145  
 QY 137 YNQRASAFACLVMIAYGVSAFFSYQAWR 166  
 DB 146 YNINVAASIFAFMTTACVGCGLGLALRRWR 175

## RESULT 11

US-10-097-340-282  
 ; Sequence 282, Application US/10097340  
 ; Publication No. US20030087250A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Monahan  
 ; APPLICANT: Manjula Gannavarapu  
 ; APPLICANT: Sebastian Hoersch  
 ; APPLICANT: Shubhangi Kamatkar  
 ; APPLICANT: Steve G. Kovats  
 ; APPLICANT: Rachel E. Meyers  
 ; APPLICANT: Michael Morrissey  
 ; APPLICANT: Peter Olandt  
 ; APPLICANT: Ami Sen  
 ; APPLICANT: Peter Veiby  
 ; APPLICANT: Gordon B. Mills  
 ; APPLICANT: Robert C. East, Jr.  
 ; APPLICANT: Karen Lu  
 ; APPLICANT: Rosemarie Schmandt  
 ; APPLICANT: Xumel Zhao  
 ; APPLICANT: Karen Glatt  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
 ; Prevention, and Therapy of Ovarian Cancer  
 ; FILE REFERENCE: MRI-030  
 ; CURRENT APPLICATION NUMBER: US/10/097,340  
 ; CURRENT FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: 60/276,025  
 ; PRIOR FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: 60/325,149  
 ; PRIOR FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: 60/276,026  
 ; PRIOR FILING DATE: 2001-03-14  
 ; PRIOR APPLICATION NUMBER: 60/324,967  
 ; PRIOR FILING DATE: 2001/09/26  
 ; PRIOR APPLICATION NUMBER: 60/311,732  
 ; PRIOR FILING DATE: 2001-08-10



```

Db      123 HENIAAVFSYIATLLVYVHVFSLIRWK 151

RESULT 15
US-09-736-457-338
; Sequence 338, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, AiJun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 338
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-338

Query Match      16.0%; Score 148.5; DB 9; Length 148;
Best Local Similarity 30.2%; Pred. No. 2.5e-07;
Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

Qy      39 ALMLQLVLGLLWALIAADTPHLYP-AYGWNFVAVFLWLVTLVFNLYLQLHMKLYM 97
Db      24 AFELPELIFGLFVMTVAAT-HIVYPLLOGWVWYVSLTSLMLFLLSYLFGFYKR--F 80
Qy      98 VPMPLVLMIFNISATVLYIT-AFIACSAAVDLTSLRGTRPYNORAAASPACLVMIAYGV 156
Db      81 ESKRVLDLSLYHGTGILYKSAAYLVQVHATVSEKLDPRYYINSAAASFFAIIATLLYL 140
Qy      157 SAFFSY 162
Db      141 HAFSIY 146

Search completed: December 1, 2004, 15:59:25
Job time : 147 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 15:40:54 ; Search time 39 Seconds  
(without alignments)  
449,012 Million cell updates/sec

Title: US-09-602-597A-4  
Perfect score: 930  
Sequence: 1 NAEFSPKSVTRTSPAQAE.....QAWRGVGSNAATSQMAGGYA 182

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: P1r1:\*  
2: P1r2:\*  
3: P1r3:\*  
4: P1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	741	79.7	157	2 A55046	plasmolipin - rat
2	158	17.0	281	2 T29464	hypothetical prote
3	153	16.5	153	2 T29472	T-cell surface gly
4	148.5	16.0	148	2 I38891	hypothetical prote
5	145.5	15.6	153	2 S68406	vesicular integral
6	141	15.2	156	2 T29152	hypothetical prote
7	95.5	10.3	242	2 T19564	hypothetical prote
8	95.5	10.3	444	2 I39294	McLeod syndrome-as
9	95	10.2	276	2 S13585	nosy protein precu
10	94.5	10.2	152	2 S32567	A4 protein - human
11	92.5	9.9	401	1 Y0ECNQ	sodium-glutamate s
12	91.5	9.8	401	2 A98195	glutamate transpor
13	91.5	9.8	401	2 B86042	glutamate transpor
14	91	9.8	208	2 T23328	hypothetical prote
15	91	9.8	379	2 D81515	cell shape-determi
16	91	9.8	415	2 A86399	rod shape protein
17	91	9.8	415	2 C72026	latent membrane pr
18	90.5	9.7	404	1 LAB8CA	probable sugar tra
19	90.5	9.7	461	2 G85059	amino acid transpo
20	90	9.7	539	2 D69748	hypothetical prote
21	89.5	9.6	202	2 B83059	hypothetical prote
22	89	9.6	264	2 E69897	hypothetical prote
23	88.5	9.5	215	2 A84008	hemolysin III BH28
24	88.5	9.5	244	2 T22046	hypothetical prote
25	88	9.5	331	2 T23504	hypothetical prote
26	87	9.4	401	2 S42583	phosphate transloc
27	87	9.4	610	2 T32917	hypothetical prote
28	86.5	9.3	400	2 A41579	beta-3-adrenergic
29	86.5	9.3	400	2 A53281	beta 3-adrenergic

# ALIGNMENTS

## RESULT 1

A55046  
plasmolipin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 18-Nov-1994 #sequence\_revision 18-Nov-1994 #text\_change 29-Sep-1999  
C:Accession: A55046  
R.Fischer, I.; Sapirstein, V.S.  
J. Biol. Chem. 269, 24912-24919, 1994  
A:Title: Molecular cloning of plasmolipin. Characterization of a novel proteolipid restr  
A:Reference number: A55046; MUID:95014262; PMID:7923173  
A:Accession: A55046  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-157 <FIS>  
A:Cross-references: GB:U13617; NID:G532799; PIDN:AAA62133.1; PID:G532800  
C:Superfamily: T-cell surface glycoprotein MAL  
C:Keywords: lipoprotein; transmembrane protein

Query Match 79.7%; Score 741; DB 2; Length 157;  
Best Local Similarity 87.9%; Pred. No. 3.6e-61;  
Matches 138; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy	26	LRPDLGFRSRIGALMLLQLVLGLLWALIAADTPHYLPAYGWYVAVFLWLTIVLFN	85
Db	1	MRPDLGFRSRIGALMLLQLVLGLLWALIAADTPHYLPAYGWYVAVFLWLTIVFFI	60
Qy	86	LYLFQLHMKLYMPWPLVLMIFNISATVLYITATACSAVDLTSLRGTRFYNORAAASF	145
Db	61	LYLFQLHMKLYMPWPLVLLVFFVAAVLYITATACSAVDLTSLRGSRFYNORAAASF	120
Qy	146	FACLVMIAYGVSAFFSYQAWRGVGSNAATSQMAGGYA	182
Db	121	FACLVMIAYGLSAPFSFOAWRGVGSNAATSQMAGGYS	157

## RESULT 2

T29464  
hypothetical protein F28H1.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29464  
R.Du, Z.; Le, T.T.  
A:Description: The sequence of C. elegans cosmid F28H1.  
A:Reference number: Z20622  
A:Accession: T29464  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-281 <DUZ>  
A:Cross-references: UNIPROT:P83386; EMBL:U97013; PIDN:AAB52340.1; GSPDB:GN00019; CESP:F2  
A:Experimental source: strain Bristol N2; clone F28H1  
C:Genetics:

A:Gene: CESP:F28H1.4

A:Map position: 1

A:Introns: 4/1; 66/3; 108/3; 150/1; 188/3; 235/3

Query Match 17.0%; Score 158; DB 2; Length 281;

Best Local Similarity 28.6%; Pred. No. 2.7e-07;

Matches 50; Conservative 27; Mismatches 76; Indels 22; Gaps 5;

QY 18 GAEASVSALRDLGFRSRLGALMLQLVGLLWVLIADTPVHLXPAYGWMVFAVFLW 77

DB 104 GPVRIEPRDCEYIRLTGIMKIVICVLLTFIFVMGPAV-YTGVGWAFVSQVI 162

QY 78 LVTIVFNLYLFQHLMKLVMPVPLVL-----MIFNISATVLYITAFIACSAV 126

DB 163 FVTSLLTLYLFRVVDLPSINWIVCLSTRTEIIFQEMVYCFATWTFPIA--ACVLAV 220

QY 127 DLTSIRGTRPNORAAAFACLVMIAYGVSAFYSQAWRG-----VGSNAATSQ 176

DB 221 ASSQFRGTFAW---AIAAFAGACAYGDCYKLFUSKNERATGGSNPVIQ 272

# RESULT 3

A29472

T-cell surface glycoprotein MAL, splice form a - human

N:Alternate names: MAL proteolipid

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004

C:Accession: A29472; S40076; S40077; S40079; S40078; A54680; I38009; S38933; S38934; S38935

R:Alonso, M.A.; Weisman, S.M.

Proc. Natl. Acad. Sci. U.S.A. 84, 1997-2001, 1987

A:Title: cDNA cloning and sequence of MAL, a hydrophobic protein associated with human T

A:Reference number: A29472; MUID: 87175600; PMID: 3494249

A:Accession: A29472

A:Molecule type: DNA

A:Residues: 1-153 <ALO>

A:Cross-references: UNIPROT:P21145; GB:M15800; NID:G187297; PIDN:AAA36196.1; PID:G307157

R:Rancano, C.; Rubio, T.; Alonso, M.A.

submitted to the EMBL Data Library, December 1993

A:Description: Alternative splicing of human T-cell specific MAL mRNA and its correlation

A:Reference number: S40076

A:Accession: S40076

A:Molecule type: mRNA

A:Residues: 1-153 <RAN>

A:Cross-references: EMBL:X76678; NID:G435477; PIDN:CAA54100.1; PID:G435478

A:Note: MAL-a

A:Accession: S40077

A:Molecule type: mRNA

A:Residues: 1-87,130-153 <RAW>

A:Cross-references: EMBL:X76679; NID:G435479; PIDN:CAA54101.1; PID:G435480

A:Note: MAL-b

A:Accession: S40079

A:Molecule type: mRNA

A:Residues: 1-31,130-153 <RAP>

A:Cross-references: EMBL:X76681; NID:G435481; PIDN:CAA54103.1; PID:G435482

A:Note: MAL-d

A:Accession: S40078

A:Molecule type: mRNA

A:Residues: 1-31,88-153 <RAA>

A:Cross-references: EMBL:X76680; NID:G435483; PIDN:CAA54102.1; PID:G435484

R:Rancano, C.; Rubio, T.; Alonso, M.A.

Genomics 21, 447-450, 1994

A:Title: Alternative splicing of human T-cell-specific MAL mRNA and its correlation with

A:Reference number: A54680; MUID: 94375076; PMID: 8088843

A:Accession: A54680

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-153 <RA2>

A:Cross-references: GB:X76678; NID:G435477; PIDN:CAA54100.1; PID:G435478

R:Rancano, C.; Rubio, T.; Correas, I.; Alonso, M.A.

J. Biol. Chem. 269, 8159-8164, 1994

A:Title: Genomic structure and subcellular localization of MAL, a human T-cell-specific

A:Reference number: I38009; MUID: 94179150; PMID: 8132541

A:Accession: I38009

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-31 <RES>

A:Cross-references: EMBL:X76220; NID:G433225; PID:G1200084

A:Experimental source: Placenta

A:Note: submitted to the EMBL Data Library, November 1993

C:Genetics:

A:Gene: GDB:MAL

A:Cross-references: GDB:119374; OMIM:188860

A:Map position: 2cen-2q13

A:Introns: 31/3; 87/3; 129/3

C:Superfamily: T-cell surface glycoprotein MAL

C:Keywords: alternative splicing; endoplasmic reticulum; glycoprotein; T-cell; transmembr

F:1-153/Product: T-cell surface glycoprotein MAL, splice form a #status predicted <MAA>

F:1-87,130-153/Product: T-cell surface glycoprotein MAL, splice form b #status predicted

F:1-31,88-153/Product: T-cell surface glycoprotein MAL, splice form c #status predicted

F:1-31,130-153/Product: T-cell surface glycoprotein MAL, splice form d #status predicted

Query Match 16.5%; Score 153; DB 2; Length 153;

Best Local Similarity 30.2%; Pred. No. 4.5e-07;

Matches 45; Conservative 25; Mismatches 61; Indels 18; Gaps 6;

QY 22 SVSALRPDLGFRSRLGALMLQLVGLLWVLIADT--PYHLYPAYGWMVFAVFLW 79

DB 17 SVFTTLPLD-----LFIFEFIFGGLVWILVASSLVPWPL--VQGWVWFSVFCFVA 65

QY 80 TIVFNLYLFQHLMKLVMPVPLVIMIFNISATVLYITAFIACSAAVDLTSLRG--TRPY 137

DB 66 TTTLLIILYIGAAGG--ETSNVTLDAVHCTAALFYLSASV-LEALATITMQDGFYRHY 122

QY 138 NORAAAFACLVMIAYGVSAFYSQAWR 166

DB 123 HENIAAVVFSYIATLLYVYVHAVFSLIRWK 151

# RESULT 4

I38891

hypotheical protein - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004

C:Accession: I38891

R:Lautner-Rieske, A.; Thiebe, R.; Zachau, H.G.

Gene 159, 199-202, 1995

A:Title: Searching for non-v kappa transcripts from the human immunoglobulin kappa locus

A:Reference number: I38891; MUID: 95347597; PMID: 7622049

A:Accession: I38891

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-148 <RBS>

A:Cross-references: UNIPROT:Q13021; EMBL:U17077; NID:G1000711; PIDN:AAA76738.1; PID:G1000

C:Genetics:

A:Gene: BENE

C:Superfamily: T-cell surface glycoprotein MAL

Query Match 16.0%; Score 148.5; DB 2; Length 148;

Best Local Similarity 30.2%; Pred. No. 1.1e-06;

Matches 38; Conservative 31; Mismatches 52; Indels 5; Gaps 4;

QY 39 ALMLQLVGLLWVLIADTPTVHLXPAYGWMVFAVFLWVLIADTPTVHLXPAYGWMVFAVFLW 97

DB 24 AFFELIFLFGVLTWVAAT--HIVYPLQGWVWVSLTSLFSLMFLSLYLFQFYKR--F 80

QY 98 VPWPLVIMIFNISATVLYIT-AFTACSAAVDLTSLRTRPYNQRAAASFPACLVMIAYGV 156

DB 81 ESWRVLSLHGTTGLYNGAALVQVHATIVSEKLDLPRIYVYNSAASFPATLTLYIL 140

QY 157 SAFFSY 162

DB 141 HAFSIY 146

# RESULT 5







Db 337 VLAAGH 342

RESULT 12

A98195

Glutamate transport protein ECs4529 [imported] - Escherichia coli (strain O157:H7, substrate) Escherichia coli

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004

C:Accession: A98195

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome reference number: A96629; MUID:21156231; PMID:11258796

A:Accession: A98195

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <HAY>

A:Cross-references: UNIPROT:Q8XD83; GB:BA000007; PIDN:BA37952.1; PID:gl3364004; GSPDB:G0509952

A:Experimental source: strain O157:H7, substrate RMD 0509952

C:Genetics:

A:Gene: ECs4529

C:Superfamily: sodium-glutamate symport carrier protein

Query Match 9.8%; Score 91.5; DB 2; Length 401;

Best Local Similarity 24.2%; Pred. No. 0.49;

Matches 45; Conservative 33; Mismatches 81; Indels 27; Gaps 6;

Qy 1 MAEPFSKYSTRSSPAQGAASVSALRDLGVRSLG-----ALMLLQVLGLLWALI 55

Db 179 VARYLVKHSHTTPNGIPDDQEVPTAFKPDVGRMTSLVLIETIALIAICLVGKIVAQLL 238

Qy 56 ADTPYHLXPAYGWMFVAVFLMLVTLVFNLYLQHLMKLYMPWPLVLMIFNISATVLY 115

Db 239 AGTAFEL-PTFVCLFVG-ILNGLSM--MGFYRVFRAVSVLGNVLSLFL 287

Qy 116 ITAFIACSRAVDLTSRGTRPNQRAAASFFACLVMIAYGVSAFYSQAWRGVGSNAATS 175

Db 288 AMALMGLK-LWELASL-----ALPMLAILVVQITFMALYAFVTRWMGKNYDAA 336

Qy 176 QMAGGY 181

Db 337 VLAAGH 342

RESULT 13

B86042

Glutamate transport [imported] - Escherichia coli (strain O157:H7, substrate EDL933)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004

C:Accession: B86042

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B86042

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <STO>

A:Cross-references: UNIPROT:Q8XD83; GB:AE005174; NID:gl2518413; PIDN:AA58798.1; GSPDB:G0509952

A:Experimental source: strain O157:H7, substrate RMD 0509952

C:Genetics:

A:Gene: GltS

C:Superfamily: sodium-glutamate symport carrier protein

Query Match 9.8%; Score 91.5; DB 2; Length 401;

Best Local Similarity 24.2%; Pred. No. 0.49;

Matches 45; Conservative 33; Mismatches 81; Indels 27; Gaps 6;

Qy 1 MAEPFSKYSTRSSPAQGAASVSALRDLGVRSLG-----ALMLLQVLGLLWALI 55

Db 179 VARYLVKHSHTTPNGIPDDQEVPTAFKPDVGRMTSLVLIETIALIAICLVGKIVAQLL 238

Qy 56 ADTPYHLXPAYGWMFVAVFLMLVTLVFNLYLQHLMKLYMPWPLVLMIFNISATVLY 115

Db 239 AGTAFEL-PTFVCLFVG-ILNGLSM--MGFYRVFRAVSVLGNVLSLFL 287

Qy 116 ITAFIACSRAVDLTSRGTRPNQRAAASFFACLVMIAYGVSAFYSQAWRGVGSNAATS 175

Db 288 AMALMGLK-LWELASL-----ALPMLAILVVQITFMALYAFVTRWMGKNYDAA 336

Qy 176 QMAGGY 181

Db 337 VLAAGH 342

RESULT 14

T23328

hypothetical protein K04G2.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T23328

R:Gardner, A. submitted to the EMBL Data Library, July 1996

A:Reference number: Z19727

A:Accession: T23328

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-208 <WIL>

A:Cross-references: UNIPROT:Q21228; EMBL:Z75712; PIDN:CA800046.1; GSPDB:GN000019; CESP:K04G2

C:Genetics:

A:Gene: CESP:K04G2.9

A:Map position: 1

A:Introns: 22/2; 57/3; 175/3

Query Match 9.8%; Score 91; DB 2; Length 208;

Best Local Similarity 24.6%; Pred. No. 0.3;

Matches 45; Conservative 30; Mismatches 76; Indels 32; Gaps 8;

Qy 8 VSTRTSPAGAAASVSAL---RPDLGFVRSRLGALMLLQVLGLLWALIADTPVHLXP 64

Db 17 VTTTREKTKYKSHSVWSGCHGPTDKNYCLGPGJLRIAEIFLCVIVLUITSV-FGPGP 75

Qy 65 AYGWVMP-----VAVFLMLVTLVFNLYLQHLMK-LYMPWPLVLMIFNISATVLY 116

Db 76 FKQ-ILFGQITLLTVASVAMLLTFILIAFYFTLHSLDFFCWFREADLLENVICAVLFI 134

Qy 117 TAFIA-----CSAAVDLTS-----LRGTRPNQRAAASFFACLVMIAYGVSAFF 160

Db 135 VLSIVEAYYSTGWSNNCN---DIGSDGIHNGCRIIYEWAFASFTLFIIGIFTALTAF 191

Qy 161 SYQ 163

Db 192 THK 194

RESULT 15

D81515

cell shape-determining protein MrdS CP1002 [imported] - Chlamydomonas reinhardtii (strain 6802) Chlamydomonas reinhardtii

C:Species: Chlamydomonas reinhardtii

C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C:Accession: D81515

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydomonas reinhardtii and Chlamydomonas reinhardtii

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: D81515

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <REA>

A:Cross-references: UNIPROT:Q9K1T9; GB:AE002257; PIDN:AE002257; PIDN:AAF3878

A:Experimental source: strain A839, HL cells

C:Genetics:

A:Gene: CPI002  
C:Superfamily: rod shape-determining protein

Query Match 9.8%; Score 91; DB 2; Length 379;  
Best Local Similarity 24.0%; Pred. No. 0.52;  
Matches 35; Conservative 24; Mismatches 49; Indels 38; Gaps 5;

Qy	23	VSALRDLGFRGRGLGAL-----MLQLVLGLLVWALADTPYHLYPAYGWMFVAVEL	76
Db	29	ISSMDPTAMLVTSKGLLTNKSIMQLRHFALGWVFFICAYFDYHLFKRWAWLY--FFM	86
Qy	77	WLVTVLFNLVLFQLHMKLYMVEW-----PLVLMIFNISATVLYITAFIACSAA	125
Db	87	ICALVGLFFVPSVQNVHRTIRPIFIHMSVQPSYKGLVVI-----MLSYILES	137
Qy	126	VDLTSLRGTRPNQRAAASFACLVN	151
Db	138	ADITS-----KTTAFACLAV	153

Search completed: December 1, 2004, 15:48:27  
Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 1, 2004, 15:28:57 ; Search time 193 Seconds  
(without alignments)  
542.581 Million cell updates/sec

Title: US-09-602-597A-4

Perfect score: 930

Sequence: 1 MAEFPKSVTRTSSPAQGAEE.....QAWRGVGSNAATSQWAGGYA 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	930	100.0	182	1	PLLP_HUMAN	Q9V342 homo sapien
2	851	91.5	182	1	PLLP_MOUSE	Q9ACU2 mus musculus
3	851	91.5	182	2	BAC27916	Bac27916 mus muscu
4	848	91.2	182	1	PLLP_RAT	P47987 rattus norv
5	323	34.7	170	2	Q6GPN9	Q6GPN9 xenopus lae
6	322	34.6	173	1	CLF8_HUMAN	Q81ZV2 homo sapien
7	316	34.0	173	1	CLF8_MOUSE	Q9CZ14 mus musculus
8	312	33.5	173	2	Q71B06	Q71B06 rattus norv
9	312	33.5	173	2	AAQ10889	Aaql0889 rattus no
10	179	19.2	174	2	Q6GNS0	Q6GNS0 xenopus lae
11	168	18.1	175	2	Q8B108	Q8B108 mus musculus
12	166.5	17.9	270	2	P83386	P83386 caenorhabdi
13	165	17.7	176	2	Q7TPB7	Q7TPB7 rattus norv
14	165	17.7	176	2	AAH62388	AAH62388 rattus no
15	162	17.4	176	1	MAL2_HUMAN	Q96912 homo sapien
16	162	17.4	176	2	Q6P1M4	Q6P1M4 homo sapien
17	162	17.4	176	2	AAH64992	AAH64992 homo sapi
18	161	17.3	159	2	Q6DER3	Q6DER3 xenopus tro
19	155	16.7	153	1	MAL_MOUSE	Q09198 mus musculus
20	155	16.7	153	2	BAB23430	Bab23430 mus muscu
21	153	16.5	153	1	MAL_HUMAN	P21145 homo sapien
22	152	16.3	153	1	MAL_RAT	Q64349 rattus norv
23	149.5	16.1	208	1	CLF4_MOUSE	Q8CJ61 mus musculus
24	148.5	16.0	153	1	BENE_HUMAN	Q13021 homo sapien
25	147.5	15.9	154	1	BENE_MOUSE	Q91X49 mus musculus
26	147.5	15.9	154	2	BAC37487	Bac37487 mus muscu
27	147.5	15.9	234	1	CLF4_HUMAN	Q81Z15 homo sapien
28	147	15.8	220	2	Q6ZMD9	Q6ZMD9 homo sapien
29	147	15.8	220	2	BAD18789	Bad18789 homo sapi
30	145.5	15.6	153	1	MAL_CANFA	Q28296 canis famil
31	144	15.5	159	2	Q6PBB5	Q6PBB5 xenopus lae

32	144	15.5	159	2	AAH59789	Aah59789 xenopus l
33	141	15.2	156	2	P83387	P83387 caenorhabdi
34	140	15.1	148	2	Q7TPB6	Q7TPB6 rattus norv
35	138.5	14.9	189	2	Q7PW02	Q7PW02 anopheles g
36	137.5	14.8	298	2	Q7Z507	Q7Z507 homo sapien
37	137.5	14.8	322	1	MYDM_HUMAN	Q96S97 homo sapien
38	137.5	14.8	322	2	BAC11513	Bac11513 homo sapi
39	137	14.7	177	2	Q9VZ71	Q9VZ71 drosophila
40	133	14.3	173	2	Q9B9K0	Q9B9K0 homo sapien
41	133	14.3	173	2	AAH62544	Aah62544 homo sapi
42	132.5	14.2	208	2	Q6DGM6	Q6DGM6 brachydanio
43	131	14.1	173	2	Q7TQC1	Q7TQC1 mus musculu
44	131	14.1	282	2	Q8BPS8	Q8BPS8 mus musculu
45	131	14.1	296	1	MYDM_MOUSE	Q35682 mus musculu

#### ALIGNMENTS

#### RESULT 1

ID	PLLP_HUMAN	STANDARD	PRT	182 AA
AC	Q9V342			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Plasmolipin.			
GN	Name=TM43F11; Synonym=PMLP;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OK	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RA	Xie B., Durie R., Sapirstein V.S.;			
RT	"Molecular cloning of human plasmolipin cDNA";			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Maman A.C., Rodriguez S., Sanchez A.,			
RA	Whiting M., Maman A.C., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schmurch A., Schein J.F., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences";			
CC	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- FUNCTION: Appears to be involved in myelination. Could also			
CC	participate in ion transport events as addition of plasmolipin to			
CC	lipid bilayers induces the formation of ion channels, which are			
CC	voltage-dependent and K(+) selective (By similarity).			
CC	-!- SUBUNIT: Hexamer arranged as a trimer of two plasmolipin subunits			
CC	(By similarity).			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-!- SIMILARITY: Belongs to the MAL family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation			

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; AF137386; AAD33060.1; -;  
EMBL; BC027600; AA027600.1; -;  
GenBank; HGNC:18553; TM4SF11.  
MIM; 600340; -;  
InterPro; IPR008253; Marvel.  
Pfam; PF01284; MARVEL; 1.  
Ion transport; Ionic channel; Transmembrane; Transport.  
DOMAIN 1 35 Cytosolic (Potential).  
TRANSMEM 36 56 Extracellular (Potential).  
DOMAIN 57 68 Potential.  
TRANSMEM 69 89 Cytosolic (Potential).  
DOMAIN 90 99 Potential.  
TRANSMEM 100 120 Extracellular (Potential).  
DOMAIN 121 141 Potential.  
TRANSMEM 142 162 Cytosolic (Potential).  
DOMAIN 163 182 Cytosolic (Potential).  
SEQUENCE 182 AA; 19986 MW; 6F09AA080E2F67E8 CRC64;

Query Match 100.0%; Score 930; DB 1; Length 182;  
Best Local Similarity 100.0%; Pred. No. 5.5e-70;  
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFPPSKVSTRSSPAQGAASVSRPDLGFRVSRGLGMLLQVLGLVLLWALIADTPY 60  
DB 1 MAFPPSKVSTRSSPAQGAASVSRPDLGFRVSRGLGMLLQVLGLVLLWALIADTPY 60  
QY 61 HLYPAYGWNVFAVFLWLTIVLFLNLYLFLQHLKLVMPVPLVLMFNISATVLYITAFI 120  
DB 61 HLYPAYGWNVFAVFLWLTIVLFLNLYLFLQHLKLVMPVPLVLMFNISATVLYITAFI 120  
QY 121 ACSAAVDLTSLRTRPNQRAAASFFACLVMIAYGVSAFFSQAVRGVGSNAATSQMAGG 180  
DB 121 ACSAAVDLTSLRTRPNQRAAASFFACLVMIAYGVSAFFSQAVRGVGSNAATSQMAGG 180  
QY 181 YA 182  
DB 181 YA 182

RESULT 2  
ID PLIP MOUSE STANDARD; PRT; 182 AA.  
AC QSDC2; (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Plasmolipin.  
GN Name=TM4SF11; Synonyms=Plmp, Plapi;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=129/SvevTACfBr; TISSUE=Spleen;  
RX MEDLINE=21564391; PubMed=11707781;  
RA Hamacher M., Pippirs U., Koehler A., Mueller H.W., Bosse F.;  
RT "Plasmolipin: genomic structure, chromosomal localization, protein  
RT expression pattern and putative association with Bardet-Biedl  
RT syndrome.";  
RL Mamm. Genome 12:933-937(2001).  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Kidney;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,  
Baldarelli R., Hill D.P., Butt C., Hume D.A., Quackenbush J.,  
Schirrell L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Blake J.A., Braggi D., Brucic V., Chothia C., Corbani L.E., Cousins S.,  
Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
Gasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,  
Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
Birney E., Hayashizaki Y.;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
Nature 420:563-573(2002).  
[3]  
SEQUENCE FROM N.A.  
TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Xie H.F.,  
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
CC -!- FUNCTION: Appears to be involved in myelination. Could also  
CC participate in ion transport events as addition of plasmolipin to  
CC lipid bilayers induces the formation of ion channels, which are  
CC voltage-dependent and K(+) selective (By similarity).  
CC -!- SUBUNIT: Hexamer arranged as a trimer of two plasmolipin subunits  
CC (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to the MAL family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; AJ298129; CAC88126.1; -;  
EMBL; AJ298130; CAC88126.1; JOINED.  
EMBL; AK002477; BAB22130.1; -;  
EMBL; BC024534; AAH24534.1; -;  
MGD; MGI:1915051; Tm4sf11.

```
DR InterPro: IPR008253; Marvel.
KW Pfam: PF01284; MARVEL; 1.
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT TRANSMEM 57 68
FT TRANSMEM 69 89
FT TRANSMEM 90 99
FT TRANSMEM 100 120
FT TRANSMEM 121 141
FT TRANSMEM 142 162
FT TRANSMEM 163 182
SQ SEQUENCE 182 AA; 19801 MW; F2D78E5E22173B42 CRC64;

Query Match 91.5%; Score 851; DB 1; Length 182;
Best Local Similarity 90.1%; Pred. No. 2.2e-63;
Matches 164; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRSRLGALMLQLVGLLWALIADTPY 60
DB 1 MAEPFSKVSTRTSSPAQGVASVSALRDLGFRSALGVLLALLQLGLLWALIADTPY 60
QY 61 HLYPAYGWMFVAVFLWLVTVIFLNLFLFOLHMKLYMPWPLVLMIFNISATVLYITAFI 120
DB 61 HLYPAYGWMFVAVFLWLVTVIFLNLFLFOLHMKLYMPWPLVLLVLIFFVAATVLYITAFI 120
QY 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSAFFSQWVRGVSNAATSQWAGG 180
DB 121 ACAAAVDLTSLRGSRPYNQRAAASFFACLVMIAYGVSAFFSQWVRGVSNAATSQWAGG 180
QY 181 YA 182
DB 181 YS 182

RESULT 3
BAC27916 PRELIMINARY; PRT; 182 AA.
AC BAC27916;
DT 14-APR-2004 (TREMELrel. 27, Created)
DT 14-APR-2004 (TREMELrel. 27, Last sequence update)
DT 14-APR-2004 (TREMELrel. 27, Last annotation update)
DE Adult male olfactory brain cDNA, RIKEN full-length enriched library,
DE clone:6430887D16 product:PLASMOLIPIN homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=22354683; PubMed=12466951;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Axiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK032540; BAC27916.1; -
SQ SEQUENCE 182 AA; 19801 MW; F2D78E5E22173B42 CRC64;

Query Match 91.5%; Score 851; DB 2; Length 182;
Best Local Similarity 90.1%; Pred. No. 2.2e-63;
Matches 164; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAEPFSKVSTRTSSPAQGAASVSALRDLGFRSRLGALMLQLVGLLWALIADTPY 60
DB 1 MAEPFSKVSTRTSSPAQGVASVSALRDLGFRSALGVLLALLQLGLLWALIADTPY 60
QY 61 HLYPAYGWMFVAVFLWLVTVIFLNLFLFOLHMKLYMPWPLVLMIFNISATVLYITAFI 120
DB 61 HLYPAYGWMFVAVFLWLVTVIFLNLFLFOLHMKLYMPWPLVLLVLIFFVAATVLYITAFI 120
QY 121 ACSAAVDLTSLRGTRPYNQRAAASFFACLVMIAYGVSAFFSQWVRGVSNAATSQWAGG 180
DB 121 ACAAAVDLTSLRGSRPYNQRAAASFFACLVMIAYGVSAFFSQWVRGVSNAATSQWAGG 180
QY 181 YA 182
DB 181 YS 182

RESULT 4
BAC27916 PRELIMINARY; PRT; 182 AA.
AC BAC27916;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Plasmolipin.
GN Name=Tm4sf11; Synonyms=Pmlp;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
```

RN  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
 RA MEDLINE=95014262; PubMed=7929173;  
 RX Fischer I., Sapirstein V.S.;  
 RA "Molecular cloning of plasmolipin. Characterization of a novel  
 RT proteolipid restricted to brain and kidney.";  
 RL J. Biol. Chem. 269:24912-24919(1994).  
 [2]  
 RN SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC STRAIN=Wistar; TISSUE=Sciatic nerve;  
 RX MEDLINE=96325522; PubMed=8714710;  
 RA Gillen C., Gleichmann M., Greiner-Petter R., Zoidl G., Kupfer S.,  
 RA Bosse F., Auer J., Mueller H.W.;  
 RT "Full-length cloning, expression and cellular localization of rat  
 RT plasmolipin mRNA, a proteolipid of PNS and CNS.";  
 RL Eur. J. Neurosci. 8:405-414(1996).  
 CC -1- FUNCTION: Appears to be involved in myelination. Could also  
 CC participate in ion transport events as addition of plasmolipin to  
 CC lipid bilayers induces the formation of ion channels, which are  
 CC voltage-dependent and K(+) selective.  
 CC -1- SUBUNIT: Hexamer arranged as a trimer of two plasmolipin subunits.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expression restricted to the sciatic nerve, in  
 CC brain and kidney. In the sciatic nerve, found in Schwann cells; in  
 CC the brain, in developing oligodendrocytes, especially of the  
 CC corpus callosum, of cortical white matter, in the optic nerve and  
 CC in the stratum radiatum and stratum oriens of the hippocampus. In  
 CC kidney, segregated to the apical surface of renal tubular  
 CC epithelia.  
 CC -1- DEVELOPMENTAL STAGE: In the sciatic nerve, first detected at  
 CC postnatal day P4, increases to a maximum at day P14 and then  
 CC declines to moderate levels in adulthood. In the brain, onset of  
 CC expression is at day P1, levels increase to reach a maximum at P20  
 CC and decline slightly to adulthood.  
 CC -1- SIMILARITY: Belongs to the MAL family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; U13617; AAA62133.1; ALT INIT.  
 DR EMBL; Z49859; CAA90017.1; -.  
 DR InterPro; IPR008253; Marvel.  
 DR Pfam; PF01284; MARVEL; 1.  
 KW Ion transport; Ionic channel; Transmembrane; Transport.  
 FT DOMAIN 1 35 Cytoplasmic (Potential).  
 FT TRANSMEM 36 56 Potential.  
 FT DOMAIN 57 68 Extracellular (Potential).  
 FT TRANSMEM 69 89 Potential.  
 FT DOMAIN 90 99 Cytoplasmic (Potential).  
 FT TRANSMEM 100 120 Potential.  
 FT DOMAIN 121 141 Extracellular (Potential).  
 FT TRANSMEM 142 162 Potential.  
 FT DOMAIN 163 182 Cytoplasmic (Potential).  
 SQ SEQUENCE 182 AA; 19833 MW; 18F5844F9AA79F6E CRC64;  
 Query Match 91.2%; Score 848; DB 1; Length 182;  
 Best Local Similarity 88.5%; Pred. No. 3.9e-63;  
 Matches 161; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MAFFPFSKVTSSPPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLVWALIADTPY 60  
 DB 1 MAFFPFSKVTSSPPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLVWALIADTPY 60  
 QY 61 HLYPAYGWNVAVFLVNLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 120  
 DB 61 HLYPAYGWNVAVFLVNLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLVFLV 120

QY 121 ACSRAVDLTSURGRTPYQNRRAAASFFACLVMIAYGVSAFTSYQAWRGVGSNAATSQMAGG 180  
 DB 121 ACAAAVDLTSURGRTPYQNRRAAASFFACLVMIAYGVSAFTSYQAWRGVGSNAATSQMAGG 180  
 QY 181 YA 182  
 DB 181 YS 182  
 RESULT 5  
 Q6GPN9 PRELIMINARY; PRT; 170 AA.  
 AC Q6GPN9;  
 DT 05-JUL-2004 (TRENBLREL. 27, Created)  
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)  
 DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg E.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
 RA Krzywinski M.I., Skalka U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917;  
 RA Klein S.L., Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073074; AAH73074.1; -.  
 DR InterPro; IPR008253; Marvel.  
 DR Pfam; PF01284; MARVEL; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 170 AA; 19221 MW; 62AB19E38DFD438C CRC64;  
 Query Match 34.7%; Score 323; DB 2; Length 170;  
 Best Local Similarity 41.5%; Pred. No. 2.6e-19;  
 Matches 66; Conservative 36; Mismatches 55; Indels 2; Gaps 2;  
 QY 8 VSTRTSPPAQGAASVSALRDLGFRVSRGLGALMLLQLVLGLVWALIADTPHYLPAYG 67  
 DB 11 VTTTSSHMETISLG-GSIAYDRSFURPTGVLLLMFGLLWALIAGSEYFLFSAFG 69







130 RKENATVINLDNRMLGNVAATIFATVTVVCGSTVLGFRWR 173

Db

## RESULT 10

Q6GNS0 PRELIMINARY; PRT; 174 AA.

AC Q6GNS0; (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI\_TaxID=8355;

[1]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RC MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RC MEDLINE=22341132; PubMed=12454917;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative";

RL Dev. Dyn. 225:384-391(2002).

[3]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RA Klein S., Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073433; AAH73433.1; -

DR InterPro; IPR008253; Marvel.

DR Pfam; PF01284; MARVEL; 1.

KW Hypothetical protein.

SQ SEQUENCE 174 AA; 18914 MW; 271P97ED7A5DECCB CRC64;

Query Match 19.2%; Score 179; DB 2; Length 174;

Best Local Similarity 29.3%; Pred. No. 2.8e-07;

Matches 48; Conservative 29; Mismatches 75; Indels 12; Gaps 3;

QY 14 SPAQGAAGSVSLRP-DLGFVSRGLGMLLQLVLVWALITADTPVHLYPAGVWVFV 72

Db 11 SPAMSYPSASVNLPTGTEVFRTYSGAFNCLIIIFGALVWILVAASNPVPVQGVWVF 70

QY 73 AVFLWLVTLVFNLYLQFLMKLVWVPLVLMFNISATVLYIFATFACSAAVDLTSI- 131

Db 71 SVTAFACSLLLLVFLTGL-VHMIQTNWNVFVLDVLAHLTAFVYFGAFVLEAAVTSILNLI 129

QY 132 -----RGRFPYQNRRAASFFACFLVMVAGVSAFFPSYQAWR 166

## RESULT 11

Q8BI08 PRELIMINARY; PRT; 175 AA.

AC Q8BI08;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length

DE enriched library, clone:9530025809 product:HYPOTHETICAL 19.1 kDa

DE PROTEIN (MAL2 PROTEOLIPID) homolog.

GN Name=Al461653;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RC MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning";

RL Meth. Enzymol. 303:19-44(1999).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RC MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection";

RL Nature 409:685-690(2001).

[3]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RC The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs";

RL Nature 420:563-573(2002).

[4]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RC MEDLINE=20499374; PubMed=11042159;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes";

RL Genome Res. 10:1617-1630(2000).

[5]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RC MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer";

RL Genome Res. 10:1757-1771(2000).

[6]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

	Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahika S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AK035986; BAC29268.1;
DR	MGI; 2145021; AI461653.
DR	GO; GO:0016020; C:membrane; IEA.
DR	InterPro; IPR008253; Marvel.
DR	Pfam; PF01284; MARVEL; 1.
DR	Hypothetical protein.
SSQ	SEQUENCE 175 AA; CE28C15CD9B6FA15.CRC64;
	Query Match 18.1%; Score 168; DB 2; Length 175; Best Local Similarity 29.3%; Pred.No.2.3e-06; Matches 44; Conservative 28; Mismatches 64; Indels 14; Gaps 3;
QY	28 PDLGFSRSLGALMLQLVLGLLVWALIADTPVHLYPAYGWVFVAFLMVLVTIVLFNLY 87     :   :     :     :     :     :     :     :     :     :
Dd	28 PDI--LATYSAGFCLIEVLGVLTWLVIASSNVPLPLLCGWMVFVSHTAFPSILLFLGLF 85     :   :     :     :     :     :     :     :     :
QY	88 LFQHLMKVMVPNPILUMINISATVLYITATIACAANDLTLSLR-----CTRP 136    : :    : :    : :    : :    : :    : :    : :    : :
Ddb	86 LSGMTQT-DANWNFLDFVVHFTVFYFGAFLEAAATSLEDLCNTTWTVKPLLNDNQ 144       :    : :    : :    : :    : :    : :    : :
QY	137 YNQRASASFACLMIAYGSVAFFSQAWR 166       :    : :    : :    : :    : :    : :    : :
Ddb	145 YNIWAIVTFAMTWATTACYGCGLAIRWR 174       :    : :    : :    : :    : :    : :    : :
	RESULT 12
RFP	P83386 PRELIMINARY; PRS; 270 AA.
ID	P83386 OOI1539; AC
AC	OI-JUL-1997 (TrEMBRel. 04, Created)
DT	01-OCT-2003 (TrEMBRel. 25, Last sequence update)
DD	01-MAR-2004 (TrEMBRel. 26, Last annotation update)
DE	Hypothesis: hypothetical protein p28H1.4.
OS	Cenorchabitis elegans.
OC	Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditoidea;
OX	Rhabditidae; Pelodirinae; Caenorhabditis. NCBI_TaxID=62339;
RN	[1]
RP	SEQUENCE FROM N.A.
RR	STRAIN=Bristol N2;
RX	MEDLINE=95069613; PubMed=9851916;
RT	Wilson R.;
RT	"Genome sequencing of the nematode C. elegans: a platform for investigating biology." The C. elegans Sequencing Consortium."
RL	Science 282:2012-2018(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RR	STRAIN=Bristol N2;
RA	Du Z., Le T.T.;
RL	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RR	STRAIN=Bristol N2;
RA	Waterston R.;
RL	Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RR	STRAIN=Bristol N2;
RA	Wilson R.;
RL	Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; U97013; AB52340.2; -.
PIR	T29464; T29464.
KOMPSP	F28H1.4; CE09769.
GO	GO:0016020; C:membrane; IEA.
InterPro	IPRO08253; Marvel.
Pfam	PF01284; MARVEL; 1.
KW	Hypothetical protein.

Db 87 LSCWVTQI-DANWNFLDFAYHVFVYFGAFLEAAATSLHDLCQNTTAVVKPLNDNQ 145

Qy 137 YNORAAASFPACLVMIAYGVSAFFSQAMR 166  
|| : || : || : || : || : ||  
Db 146 YNINVAATVEAFMTTACYGCSLCLALRRWR 175

RESULT 15

ID	MAL2 HUMAN	STANDARD;	PRT;	176 AA.
AC	Q969L2;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	MAL2 protein.			
DN	Name=MAL2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH TPDS2L2.			
RX	MEDLINE=21433826; PubMed=11549320; DOI=10.1106/geno.2001.6610;			
RA	Wilson S.H.D., Bailey A.M., Nourse C.R., Mattei M.-G., Byrne J.A.;			
RT	"Identification of MAL2, a novel member of the mal proteolipid family,			
RT	though interactions with TPDS2-like proteins in the yeast two-hybrid			
RL	system";			
RN	Ganomics 76:81-88(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Ovary;			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Munry D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalus D.E.,			
RA	Schmerch A., Schein J.E., Jones S.C.M., Marra W.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences.";			
RI	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
CC	-!- SUBUNIT: Interacts with TPDS2L2.			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-!- TISSUE SPECIFICITY: Predominantly expressed in kidney, lung, and			
CC	liver.			
CC	-!- SIMILARITY: Belongs to the MAL family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AY007723; AAC15576.1; "			
DR	EMBL; BC012367; AAH12367.1; "			
DR	Genew; HGNC:13634; MAL2.			
DR	InterPro; IPR008253; Marvel.			
DR	Pfam; PF01284; MARVEL; 1.			
KW	Transmembrane.			
FT	TRANSMEM 35 .. 55 Potential.			

FT TRANSMEM 67 87 Potential.  
FT TRANSMEM 103 123 Potential.  
FT TRANSMEM 150 170 Potential.  
SQ SEQUENCE 176 AA; 19125 MW; BACDA0BF3A26FD44 CRC64;  
Query Match 17.4%; Score 162; DB 1; Length 176;  
Best Local Similarity 28.7%; Pred. No. 7.4e-06;  
Matches 43; Conservative 30; Mismatches 63; Indels 14; Gaps 4;  
Qy 28 PDIGFVRSRLGALLQLVLGLLWALIADTPHLYPAYGNWVAVFLMLVTIVLNL 87  
Db 29 PDI--LRTYSGAFVCLBLEFGLWLVIVASSNVLPFLQGNWVSVTAFVFFSLFLGMF 86  
Qy 88 LFOLEMKLYMVPWPLVLMIFNISATVLYITAFIACSAVDL-----TSLRG-----TRP 136  
Db 87 LSGNVAOI-DANNFLDFAYHFTVFYFGAFLEAAATSLHDLHCNTTITGQPLLSDNQ 145  
Qy 137 YNQRAAASFACLVMIAYGVSAFFSYQAWR 166  
Db 146 YNINVAASIFAFTTACVCGSLGLALRRWR 175

Search completed: December 1, 2004, 15:46:57  
Job time : 195 secs